PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68 | A2

(11) International Publication Number: **WO 98/50555**

(43) International Publication Date: 12 November 1998 (12.11.98)

(21) International Application Number: PCT/US98/08985

(22) International Filing Date: 4 May 1998 (04.05.98)

(30) Priority Data:

60/044,031	6 May 1997 (06.05.97)	US
60/046,655	16 May 1997 (16.05.97)	US
60/066,009	14 November 1997 (14.11.97)	US

(71) Applicant *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: KUNSCH, Charles, A. [US/US]; 4083 Spalding Hollow, Norcross, GA 30092 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US).

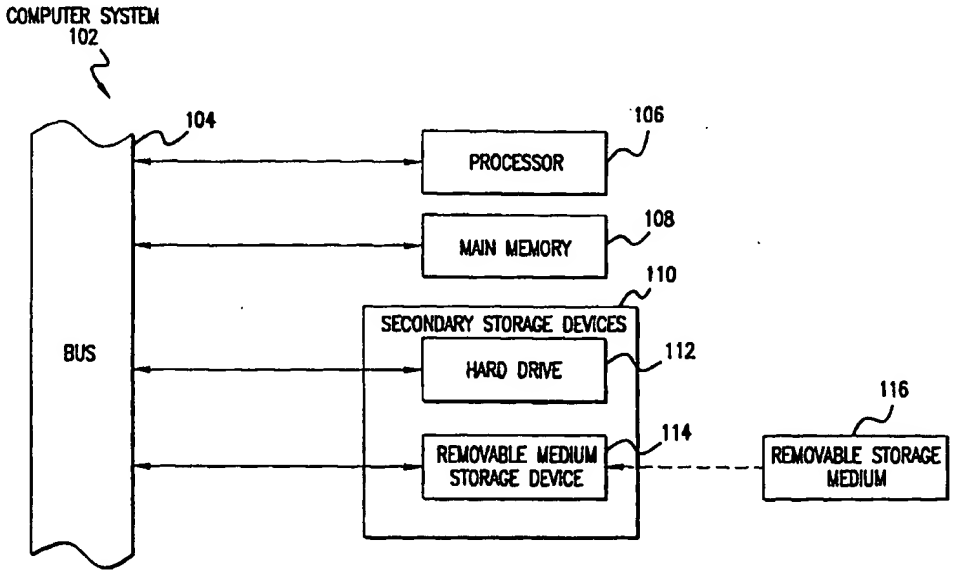
(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

(54) Title: *ENTEROCOCCUS FAECALIS* POLYNUCLEOTIDES AND POLYPEPTIDES



(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Enterococcus faecalis*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	**ES**	Spain	**LS**	Lesotho	**SI**	Slovenia
AM	Armenia	**FI**	Finland	**LT**	Lithuania	**SK**	Slovakia
AT	Austria	**FR**	France	**LU**	Luxembourg	**SN**	Senegal
AU	Australia	**GA**	Gabon	**LV**	Latvia	**SZ**	Swaziland
AZ	Azerbaijan	**GB**	United Kingdom	**MC**	Monaco	**TD**	Chad
BA	Bosnia and Herzegovina	**GE**	Georgia	**MD**	Republic of Moldova	**TG**	Togo
BB	Barbados	**GH**	Ghana	**MG**	Madagascar	**TJ**	Tajikistan
BE	Belgium	**GN**	Guinea	**MK**	The former Yugoslav Republic of Macedonia	**TM**	Turkmenistan
BF	Burkina Faso	**GR**	Greece			**TR**	Turkey
BG	Bulgaria	**HU**	Hungary	**ML**	Mali	**TT**	Trinidad and Tobago
BJ	Benin	**IE**	Ireland	**MN**	Mongolia	**UA**	Ukraine
BR	Brazil	**IL**	Israel	**MR**	Mauritania	**UG**	Uganda
BY	Belarus	**IS**	Iceland	**MW**	Malawi	**US**	United States of America
CA	Canada	**IT**	Italy	**MX**	Mexico	**UZ**	Uzbekistan
CF	Central African Republic	**JP**	Japan	**NE**	Niger	**VN**	Viet Nam
CG	Congo	**KE**	Kenya	**NL**	Netherlands	**YU**	Yugoslavia
CH	Switzerland	**KG**	Kyrgyzstan	**NO**	Norway	**ZW**	Zimbabwe
CI	Côte d'Ivoire	**KP**	Democratic People's Republic of Korea	**NZ**	New Zealand		
CM	Cameroon			**PL**	Poland		
CN	China	**KR**	Republic of Korea	**PT**	Portugal		
CU	Cuba	**KZ**	Kazakstan	**RO**	Romania		
CZ	Czech Republic	**LC**	Saint Lucia	**RU**	Russian Federation		
DE	Germany	**LI**	Liechtenstein	**SD**	Sudan		
DK	Denmark	**LK**	Sri Lanka	**SE**	Sweden		
EE	Estonia	**LR**	Liberia	**SG**	Singapore		

Enterococcus faecalis Polynucleotides and Polypeptides

FIELD OF THE INVENTION

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Enterococcus faecalis*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

BACKGROUND OF THE INVENTION

Enterococci have been recognized as being pathogenic for humans since the turn of the century when they were first described by Thiercelin in 1988 as microscopic organisms. The genus Enterococcus includes the species Enterococcus faecalis or *E. faecalis* which is the most common pathogen in the group, accounting for 80 - 90 percent of all enterococcal infections. *See* Lewis et al. (1990) Eur J. Clin Microbiol Infect Dis. 9:111-117.

The incidence of enterococcal infections has increased in recent years and enterococci are now the second most frequently reported nosocomial pathogens. Enterococcal infection is of particular concern because of its resistance to antibiotics. Recent attention has focused on enterococci not only because of their increasing role in nosocomial infections, but also because of their remarkable and increasing resistance to antimicrobial agents. These factors are mutually reinforcing since resistance allows enterococci to survive in an environment in which antimicrobial agents are heavily used; the hospital setting provides the antibiotics which eliminate or suppress susceptible bacteria, thereby providing a selective advantage for resistant organisms, and the hospital also provides the potential for dissemination of resistant enterococci via the usual routes of hand and environmental contamination.

Antimicrobial resistance can be divided into two general types, inherent or intrinsic property and that which is acquired. The genes for intrinsic resistance, like other species characteristics, appear to reside on the chromosome. Acquired resistance results from either a mutation in the existing DNA or acquisition of new DNA. The various inherent traits expressed by enterococci include resistance to semisynthetic penicillinase-resistant penicillins, cephalosporins, low levels of aminoglycosides, and low levels of clindamycin. Examples of acquired resistance include resistance to

chloramphenicol, erythromycin, high levels of clindamycin, tetracycline, high levels of aminoglycosides, penicillin by means of penicillinase, fluoroquinolones, and vancomycin. Resistance to high levels of penicillin without penicillinase and resistance to fluoroquinolones are not known to be plasmid or transposon mediated and presumably are due to mutation(s).

Although the main reservoir for enterococci in humans is the gastrointestinal tract, the bacteria can also reside in the gallbladder, urethra and vagina.

E. faecalis has emerged as an important pathogen in endocarditis, bacteremia, urinary tract infections (UTIs), intraabdominal infections, soft tissue infections, and neonatal sepsis (Lewis 1990, *supra*). In the 1970s and 1980s enterococci became firmly established as major nosocomial pathogens. They are now the fourth leading cause of hospital-acquired infection and the third leading cause of bacteremia in the United States. Fatality ratios for enterococcal bactermia range from 12% to 68%, with death due to enterococcal sepsis in 4 to 50% of these cases. *See* Emori, T.G. (1993) Clin. Microbiol. Rev. 6:428-442.

The ability of enterococci to colonize the gastrointestinal tract, plus the many intrinsic and acquired resistance traits, means that these organisms, which usually seem to have relatively low intrinsic virulence, are given an excellent opportunity to become secondary invaders. Since nosocomial isolates of enterococci have displayed resistance to essentially every useful antimicrobial agent, it will likely become increasingly difficult to successfully treat and control enterococcal infections. Particularly when the various resistance genes come together in a single strain, an event almost certain to occur at some time in the future.

The etiology of diseases mediated or exacerbated by Enterococcus faecalis, involves the programmed expression of *E. faecalis* genes, and that characterizing these genes and their patterns of expression would dramatically add to our understanding of the organism and its host interactions. Knowledge of the *E. faecalis* gene and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, treating and diagnosing diseases. Thus, there is a need to characterize the genome of *E. faecalis* and for polynucleotides of this organism.

SUMMARY OF THE INVENTION

The present invention is based on the sequencing of fragments of the *Enterococcus faecalis* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS:1-982.

The present invention provides the nucleotide sequence of hundreds of contigs of the *Enterococcus faecalis* genome, which are listed in tables below and set out in the

Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS:1-982.

The present invention further provides nucleotide sequences which are at least 95%, 96%, 97%, 98%, and 99%, identical to the nucleotide sequences of SEQ ID NOS:1-982.

The nucleotide sequence of SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-982 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Enterococcus faecalis* genome.

Another embodiment of the present invention is directed to fragments of the *Enterococcus faecalis* genome having particular structural or functional attributes. Such fragments of the *Enterococcus faecalis* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs, fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression modulating fragments or EMFs, and fragments which can be used to diagnose the presence of *Enterococcus faecalis* in a sample, hereinafter referred to as diagnostic fragments or DFs.

Each of the ORFs in fragments of the *Enterococcus faecalis* genome disclosed in Tables 1-3, and the EMFs found 5' prime of the initiation codon, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Enterococcus faecalis* genome of the present invention. The

recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Enterococcus faecalis* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Enterococcus faecalis* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated polypeptides and proteins encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention from cells which have been altered to express them.

The invention further provides methods of obtaining homologs of the fragments of the *Enterococcus faecalis* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising

one of the antibodies, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a)contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b)determining whether the agent binds to said protein.

The present genomic sequences of *Enterococcus faecalis* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Enterococcus faecalis* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Enterococcus faecalis* researchers and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

DESCRIPTION OF THE FIGURES

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of the present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Enterococcus faecalis* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of

sequence files. The program Sequis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Enterococcus faecalis* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using Extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed by seq_filter to trim portions of the sequences with more than 1% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with GeneMark, described in Borodovsky, M. and McIninch, J.D. (1993) *Comput. Chem.*, 17:123133. The ORFs are searched against *E. faecalis* sequences from GenBank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al., J. Mol. Biol. 215:* 403-410 (1990)). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention is based on the sequencing of fragments of the *Enterococcus faecalis* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS: 1-982. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Enterococcus faecalis* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS: 1-982 , or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-982" refers to any portion of the SEQ ID NOS: 1-982 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Enterococcus faecalis* open reading frames (ORFs), expression modulating fragment (EMFs) and fragments which can be used to diagnose the presence of *Enterococcus faecalis* in a sample (DFs). A non-limiting identification of preferred representative fragments is provided in Tables 1-3. As discussed in detail below, the information provided in SEQ ID NOS:1-982 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the

art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Enterococcus faecalis* proteins.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1-3 and SEQ ID NOS:1-982, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in SEQ ID NOS:1-982 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of SEQ ID NOS:1-982 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of SEQ ID NOS:1-982 wherein the contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in SEQ ID NOS:1-982. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, of each SEQ ID NO:, are included in the invention.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of SEQ ID NOS:1-982. Any number of fragments of nucleotide sequences in SEQ ID NOS:1-982, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

While the presently disclosed sequences of SEQ ID NOS:1-982 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide

sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-982. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS:1-982 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS: 1-982 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotides may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS: 1-982 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-982.

As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. A wide variety of *Enterococcus faecalis* strains that can be used to prepare *E. faecalis* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). While the present invention is enabled by the sequences and other information herein disclosed, the *E. faecalis* strain that provided the DNA of the present Sequence Listing, Strain V586, kindly provided by Dr. Michael Gilmore, University of Oklahoma, has been deposited in the ATCC, as a convenience to those of skill in the art. The *E. faecalis* strain V586 was deposited 2 May 1997 at the ATCC, 10801 University Blvd. Manassas, VA 20110-2209, and given accession number 55969. The provision of the deposits is not a waiver of any rights of the inventors or their assignees in the present subject matter.

The nucleotide sequences of the genomes from different strains of *Enterococcus faecalis* differ somewhat. However, the nucleotide sequences of the genomes of all *Enterococcus faecalis* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS: 1-982. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

The present application is further directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in SEQ ID NOS:

1-982. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *E. faecalis* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *E. faecalis* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *E. faecalis* activity include, *inter alia*, isolating an *E. faecalis* gene or allelic variants thereof from a DNA library, and detecting *E. faecalis* mRNA expression samples, environmental samples, suspected of containing *E. faecalis* by Northern Blot analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in SEQ ID NOS: 1-982, which do, in fact, encode a polypeptide having *E. faecalis* protein activity By "a polypeptide having *E. faecalis* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in SEQ ID NOS: 1-982 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 1 and 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Tables 1 and 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that

the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *E. faecalis* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in SEQ ID NOS: 1-982, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the presence invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See* Brutlag et al. (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

COMPUTER RELATED EMBODIMENTS

The nucleotide sequences provided in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS:1-982 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.*, a nucleotide sequence provided in SEQ ID NOS:1-982 , a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-982. Such a manufacture provides a large portion of the *Enterococcus faecalis* genome and parts thereof (*e.g.*, a *Enterococcus faecalis* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *Enterococcus faecalis* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD- ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily

appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially- available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a sequence of SEQ ID NOS: 1-982 the present invention enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem. 17*:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Enterococcus faecalis* genome which contain homology to ORFs or proteins from both *Enterococcus faecalis* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Enterococcus faecalis* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful

metabolites, proteins to be used as vaccines or in the generation of immuno-therapeutic reagents, or as drug screening targets.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Enterococcus faecalis* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer- based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBI). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important

fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Enterococcus faecalis* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Enterococcus faecalis* genome. In the present examples, implementing software which implement the BLAST algorithm, described in Altschul *et al.* (1990) *J. Mol. Biol. 215:* 403-410, is used to identify open reading frames within the *Enterococcus faecalis* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing and processing the genomic sequence (such as search tools, comparing tools, *etc.*) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to isolated fragments of the *Enterococcus faecalis* genome. The fragments of the *Enterococcus faecalis* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Enterococcus faecalis* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Enterococcus faecalis* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-982, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Enterococcus faecalis* DNA can be enzymatically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate a *Enterococcus faecalis* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS:1-982. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library or *Enterococcus faecalis* genomic DNA. Thus, given the availability of SEQ ID NOS:1-982, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-982 using methods set out above, those of skill will be enabled by the present

disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA. As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein. Each sequence of SEQ ID NOS:1-982, however, begins and ends with a termination codon. For purposes of numbering and reference to polynucleotide and polypeptide sequences the entire sequence of each sequence of SEQ ID NOS:1-982 is included with the first nucleotide being positon 1. Therefore, for reference purposes the numbering used in the present invention is that provided in the sequence listing for SEQ ID NOS:1-982.

Tables 1, 2, and 3 list ORFs in the *Enterococcus faecalis* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive, or more selective lists.

Table 1 sets out ORFs in the *Enterococcus faecalis* contigs of the present invention that over a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis) to a nucleotide sequence available through GenBank in March, 1997.

Table 2 sets out ORFs in the *Enterococcus faecalis* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in March, 1997.

Table 3 sets out ORFs in the *Enterococcus faecalis* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in March, 1997.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the coordinate of the first nucleotide of the ORF, counting from the 5' end of the contig strand; the fourth column indicates the coordinate of the final nucleotide of the ORF, counting from the 5' end of the contig strand.

In Tables 1 and 2, column five lists the Reference for the closest matching sequence available through GenBank. These reference numbers are the database entry numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column six in Tables 1 and 2 provides the gene name of the matching sequence.

In Table 1, column seven provides the nucleotide BLAST percent identity score from the comparison of the ORF and the GenBank sequence, column eight indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis, and column nine provides the total length of the ORF in nucleotides.

In Table 2, column seven provides the protein BLAST percent similarity of the highest scoring segment pair identified, column eight provides the percent identity of the highest scoring segment pair, and column nine provides the total length of the ORF in nucleotides.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list percent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the percent identity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Enterococcus faecalis* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Enterococcus faecalis* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment,

or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Enterococcus faecalis* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Enterococcus faecalis* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Enterococcus faecalis* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 99% and preferably 99.9% identical to SEQ ID NOS:1-982, with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the

coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Enterococcus faecalis* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORFs of the *Enterococcus faecalis* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5 to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particularly *Enterococcus faecalis*. Especially preferred in this regard are ORFs such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Enterococcus faecalis*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Enterococcus faecalis*, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*:1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem. 56*:560 (1991) and *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Enterococcus faecalis* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention

comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Enterococcus faecalis* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBS SK (+ or -), pBS KS (+ or -), pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Enterococcus faecalis* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.*, BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Enterococcus faecalis* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can

be used to produce a heterologous protein under the control of the EMF. The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. Preferred polypeptides and proteins of the present invention are polypeptides and proteins coded for by the polynucleotides of SEQ ID NOS:1-982, wherein the polypeptides and proteins are coded in the same frame as the termination codon at the end of each sequence of SEQ ID NOS:1-982. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the *E. faecalis* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in the art of protein purification.

The invention further provides for isolated *E. faecalis* polypeptides comprising an amino acid sequence selected from the group including: (a) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence from the first methionine codon to the termination codon of each sequence listed in SEQ ID NOS:1-982, wherein said termination codon is at the end of each SEQ ID NO: and said first methionine is the first methionine in frame with said termination codon; and (b) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence in (a) excepting the N-terminal methionine.

The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a) and (b) above.

The present invention is further directed to polynucleotide encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences described herein, are at least 5 contiguous amino acid in length, are selected from any two integers, one of which representing a N-terminal position. The initiation codon of the polypeptides of the present inventions position 1. The initiation codon (positon 1) for purposes of the present invention is the first methionine codon of each sequence of SEQ ID NOS:1-982 which is in frame with the termination codon at the end of each said sequence. Every combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given amino acid sequence encoded by a sequence of SEQ ID NOS:1-982 is included in the invention, i.e., from initiation codon up to the termination codon. At least means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in a full length amino acid sequence minus 1. Therefore, included in the invention are contiguous fragments specified by any N-terminal and C-terminal positions of amino acid sequence set forth in SEQ ID NOS:1-982 wherein the contiguous fragment is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in a full length sequence minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

Further polypeptides of the present invention include polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *E. faecalis* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *E. faecalis* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the

reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequences encoded by the sequences of SEQ ID NOS:1-982, as described hererin, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the

sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual corrections are to made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present invention that do not have *E. faecalis* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *E. faecalis* protein expression or as agonists and antagonists capable of enhancing or inhibiting *E. faecalis* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *E. faecalis* protein binding proteins which are also candidate agonists and antagonists according to the present invention. *See, e.g.,* Fields et al. (1989) Nature 340:245-246.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*,

E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Enterococcus faecalis* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

Recombinant expression vehicle or "vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancer and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *E. coli*, *B. subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas* and *Streptomyces*. Others may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available form Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell 23:*175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5 flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Enterococcus faecalis*, of the fragments of the *Enterococcus faecalis* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Enterococcus faecalis* is defined as a homolog of a fragment of the *Enterococcus faecalis* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Enterococcus faecalis* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the

sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among those are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-982 or from a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS:1-982 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have been described in great detail in many publications such as, for example, Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS:1-982 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS: 1-982, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C in 6X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NOS:1-982, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-982, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Enterococcus faecalis*.

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Enterococcus faecalis* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., MacMillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESES, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Enterococcus faecalis* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-982.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*, *Symbiosis 21*:79 (1986) and Voragen *et al.* in *Biocatalysts In Agricultural Biotechnology*, Whitaker *et al.*, Eds., *American Chemical Society Symposium Series 389*:93 (1989) .

The metabolism of sugars is an important aspect of the primary metabolism of *Enterococcus faecalis*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al.*, *Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters 1*:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.*, beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.*, Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al.*, *Biochem. et Biophysica. Acta. 872*:83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, Starch *40*:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, Acid Proteases Structure Function and Biology, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, Industrial Enzymes, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, Report Industrial Enzymes by 1990, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London 310*:227 (1985) and Poserke, *Journal of the American Oil Chemist Society 61*:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high

catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology 136*:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein.

E. faecalis protein-specific antibodies for use in the present invention can be raised against the intact *E. faecalis* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')2 and other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *E. faecalis* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')2 fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, *E. faecalis* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA

technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *E. faecalis* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *E. faecalis* polypeptide-specific antibody can be blocked by the *E. faecalis* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *E. faecalis* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *E. faecalis* polypeptide-specific antibodies.

Antibodies and fragements thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragements of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragements discussed above., i.e, by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particuarlly discribed fragement of a polypeptide of the present invention and allows for the exclusion of the same.

Antibodies and fragements thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragements that do not bind polypeptides of any other species of *Enterococcus* other than *E. faecalis* are included in the present invention. Likewise, antibodies and fragements that bind only species of *Enterococcus*, i.e. antibodies and fragements that do not bind bacteria from any genus other than *Enterococcus*, are included in the present invention.

3. Diagnostic and Detection Assays and Kits

The present invention further relates to methods for assaying enterococcal infection in an animal by detecting the expression of genes encoding enterococcal polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Enterococcus*-specific antibodies, nucleic acids, or proteins. Analysis of nucleic acid specific to *Enterococcus* is assayed by PCR or hybridization

techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. *See, e.g.,* Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Eremeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids *via* PCR).

Where diagnosis of a disease state related to infection with *Enterococcus* has already been made, the present invention is useful for monitoring progression or regression of the disease state whereby patients exhibiting enhanced *Enterococcus* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Enterococcus* polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Enterococcus* polypeptides or nucleic acids. Methods for obtaining biological samples such as tissue are well known in the art.

The present invention is useful for detecting diseases related to *Enterococcus* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Enterococcus* polypeptides having sufficient homology to the nucleic acid sequences identified in SEQ ID NOS:1-982 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium

phosphate buffer. A *E. faecalis* polynucleotide sequence shown in SEQ ID NOS:1-982 labeled according to any appropriate method (such as the ^{32}P-multiprimed DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *E. faecalis* DNA sequence of the present invention is used as a template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (*i.e.*, mRNA encoding *Enterococcus* polypeptides).

Levels of mRNA encoding *Enterococcus* polypeptides are assayed, for *e.g.*, using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Enterococcus* polypeptides of the present invention) are quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Enterococcal species including *E. faecalis* using bio chip technology. The present invention includes both high density chip arrays (>1000 oligonucleotides per cm^2) and low density chip arrays (<1000

oligonucleotides per cm^2). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. The bio chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips can also be used to monitor an *E. faecalis* or other Enterococcal infections and to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in the same manner as for the fragements, i.e, by their 5' and 3' positions or length in contigious base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681, 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *E. faecalis* or other Enterococcal species and infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using biosenors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Enterococcus* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Enterococcus* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody

(polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Enterococcus* polypeptides for Western-blot or dot/slot assay. *See, e.g.,* Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell . Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Enterococcus* polypeptide can be accomplished using an isolated *Enterococcus* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Enterococcus* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Enterococcus* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify a *Enterococcus* polypeptide. The amount of a *Enterococcus* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Enterococcus* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Enterococcus* polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include radioisotopes, such as iodine (^{125}I, ^{121}I), carbon

(^{14}C), sulphur (^{35}S), tritium (^{3}H), indium (^{112}In), and technetium (^{99m}Tc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Enterococcus* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include malate dehydrogenase, Enterococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include ^{3}H, ^{111}In, ^{125}I, ^{131}I, ^{32}P, ^{35}S, ^{14}C, ^{51}Cr, ^{57}To, ^{58}Co, ^{59}Fe, ^{75}Se, ^{152}Eu, ^{90}Y, ^{67}Cu, ^{217}Ci, ^{211}At, ^{212}Pb, ^{47}Sc, ^{109}Pd, etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since its avoids the problem of dehalogenation of the ^{125}I or ^{131}I-labeled monoclonal antibody by the liver. In addition, this radionucleotide has a more favorable gamma emission energy for imaging.. *See, e.g.,* Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd, ^{55}Mn, ^{162}Dy, ^{52}Tr, and ^{56}Fe.

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977) Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *E. faecalis* infection. Such a kit may include an isolated *E. faecalis* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*E. faecalis* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *E. faecalis* antigen can be detected by binding of the reporter labeled antibody to the anti-*E. faecalis* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *E. faecalis* infection in a subject. This detection method includes reacting a body fluid, preferably serum, from the subject with an isolated *E. faecalis* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein , typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Enterococcal species including *E. faecalis* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Enterococcal species, including *E. faecalis*. Bio chip and biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Enterococcal species, including *E. faecalis* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect

Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

The bio chips of the present invention may further comprise polypeptide sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragements thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the antibodies or fragements thereof of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *E. faecalis* or other Enterococcal infection and to monitor the genetic changes (amio acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention may be specified in the same manner as for the fragements, i.e, by their N-terminal and C-terminal positions or length in contigious amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Enterococcal species, including *E. faecalis*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos. and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Enterococcus faecalis* fragment and contigs herein described.

In general, such methods comprise steps of:

(a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Enterococcus faecalis* genome; and

(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides," in *Synthetic Peptides, A User's Guide*, W. H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry 28:*9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res. 6:*3073 (1979); Cooney *et al.*, *Science 241:*456 (1988); and Dervan *et al.*, *Science 251:*1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56:*560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression,* CRC Press, Boca Raton, FL (1988)). Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences

of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

5. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Enterococcus faecalis*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth and/or pathogenicity of *Enterococcus faecalis* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components are well known in the art.

As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most

cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.*, inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to

control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *E. faecalis* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be more effective in eliciting protective immune responses against multiple species and strains of the *Enterococcus* genus than single polypeptide vaccines.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. *See, e.g.*, Decker et al. (1996) J. Infect. Dis. 174:S270-275. In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. *See, e.g.*, Aristegui, J. et al. (1997) Vaccine 15:7-9.

The present invention in addition to single-component vaccines includes multi-component vaccines. These vaccines comprise more than one polypeptide, immunogen or antigen. Thus, a multi-component vaccine would be a vaccine comprising more than one of the *E. faecalis* polypeptides of the present invention.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *E. faecalis* polypeptides described in SEQ ID NOS:1-982. For example, the *E.*

faecalis polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *E. faecalis* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing heterologous proteins are known in the art. *See, e.g.*, Robinson, K. et al. (1997) Nature Biotech. 15:653-657; Sirard, J. et al. (1997) Infect. Immun. 65:2029-2033; Chabalgoity, J. et al. (1997) Infect. Immun. 65:2402-2412 . These cells may be administered live or may be killed prior to administration. Chabalgoity, J. et al., *supra*, for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *E. faecalis* polypeptides of the present invention, or fragments thereof, with additional non-Enterococcal components (*e.g.*, diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Enterococcus* genus and non-Enterococcal pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA vaccines are currently being developed for a number of infectious diseases. *See, et al.*, Boyer, et al. (1997) Nat. Med. 3:526-532; reviewed in Spier, R. (1996) Vaccine 14:1285-1288. Such DNA vaccines contain a nucleotide sequence encoding one or more *E. faecalis* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. For example, the direct administration of plasmid DNA encoding *B. burgdorgeri* OspA has been shown to elicit protective immunity in mice against borrelial challenge. *See,* Luke et al. (1997) J. Infect. Dis. 175:91-97.

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim et al. (1997) Nature Biotech. 15:641-646, for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves. These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to Enterococcal infection by either passive or active immunization. When the vaccines of

the present invention are used to confer resistance to Enterococcal infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a Enterococcal infection. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Enterococcus* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating Enterococcal infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *E. faecalis* polypeptides disclosed herein, or fragments thereof, as well as other *Enterococcus* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Enterococcus* cells, toxin moieties will be localized to these cells and will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a Enterococcal infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compound(s) are provided in advance of any symptoms of Enterococcal infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Enterococcus* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *E. faecalis* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and

carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

A composition is said to be "pharmacologically or physiologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *E. faecalis* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and incomplete), mineral salts (for example, $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*. Other substances useful as adjuvants are the saponins such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $AlK(SO_4)_2$, $AlNa(SO_4)_2$, and $AlNH_4(SO_4)$.

Examples of materials suitable for use in vaccine compositions are provided in REMINGTON'S PHARMACEUTICAL SCIENCES 1324-1341 (A. Osol, ed, Mack Publishing Co, Easton, PA, (1980) (incorporated herein by reference).

The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharangeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide). *See*, Shahin, R. et al. (1995) Infect. Immun. 63:1195-1200. Similarly, orally administered encapsulated *Salmonella typhimurium* antigens can also be used. Allaoui-Attarki, K. et al. (1997) Infect. Immun. 65:853-857. Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of

the invention can vary from 0.01-1,000 μg/ml per dose, more preferably 0.1-500 μg/ml per dose, and most preferably 10-300 μg/ml per dose.

6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large genome can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics 2*:231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P0, that any given base in a sequence of size L, in nucleotides, is not sequenced after a certain amount, n, in nucleotides, of random sequence has been determined can be calculated by the equation P0 = e-m, where m is L/n, the fold coverage. For instance, for a genome of 2.8 Mb, m=1 when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, P0 = e-1 = 0.37. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L, in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G, is determined by the equation G = Le-m, and the average gap size, g, follows the equation, g = L/n. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Enterococcus faecalis DNA is prepared by phenol extraction. A mixture containing 200 µg DNA in 1.0 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 50% glycerol is processed through a nebulizer (IPI Medical Products) with a stream of nitrogen adjusted to 35 Kpa for 2 minutes. The sonicated DNA is ethanol precipitated and redissolved in 500 µl TE buffer.

To create blunt-ends, a 100 µl aliquot of the resuspended DNA is digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 µl BAL31 buffer. The digested DNA is phenol-extracted, ethanol-precipitated, redissolved in 100 µl TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size is excised from the gel, and the LGT agarose is melted and the resulting solution is extracted with phenol to separate the agarose from the DNA. DNA is ethanol precipitated and redissolved in 20 µl of TE buffer for ligation to vector.

A two-step ligation procedure is used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 ul) contains 2 µg of DNA fragments, 2 µg pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and is incubated at 14°C for 4 hr. The ligation mixture then is phenol extracted and ethanol precipitated, and the precipitated DNA is dissolved in 20 µl TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder are visualized by ethidium bromide-staining and UV illumination and identified by size as insert (I), vector (v), v+I, v+2i, v+3i, *etc.* The portion of the gel containing v+I DNA is excised and the v+I DNA is recovered and resuspended into 20 µl TE. The v+I DNA then is blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50 ul) containing the v+I linears, 500 µM each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+I linears are dissolved in 20 µl TE. The final ligation to produce circles is carried out in a 50 µl reaction containing 5 µl of v+I linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture is stored at -20°C.

This two-stage procedure results in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, *E. coli* host cells deficient in all recombination and restriction functions (A. Greener, *Strategies 3 (1)*:5 (1990)) are used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells are plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating is carried out as follows. A 100 µl aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) is thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 µl aliquot of 1.42 M beta-mercaptoethanol is added to the aliquot of cells to a final concentration of 25 mM. Cells are incubated on ice for 10 min. A 1 µl aliquot of the final ligation is added to the cells and incubated on ice for 30 min. The cells are heat pulsed for 30 sec. at 42°C and placed back on ice for 2 min. The outgrowth period in liquid culture is eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture is plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml MgCl2 (1 M), and 1 ml MgSO4/100 ml SOB agar. The 15 ml top layer is poured just prior to plating. Our titer is approximately 100 colonies/10 µl aliquot of transformation.

All colonies are picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products are deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates are prepared using a "boiling bead" method developed in collaboration with Advanced Genetic Technology Corp. (Gaithersburg, MD) (Adams *et al.*, *Science 252*:1651 (1991); Adams *et al.*, *Nature 355*:632 (1992)). Plasmid preparation is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration is determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations are not adjusted, but low-yielding templates are identified where possible and not sequenced.

Templates are also prepared from an *Enterococcus faecalis* lambda genomic library in the vector DASH II (Stratagene). In particular, *Enterococcus faecalis* DNA (> 100 kb) is partially digested in a reaction mixture (200 ul) containing 50 µg DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23°C. The digested DNA was phenol-extracted and fractionated by sucrose density gradient centrifugation. Fractions of the sucrose gradient containing 15 to 25 kb are recovered in a final volume of 6 ul. One µl of fragments is used with 1 µl of lambda DASHII vector (Stratagene) in the recommended ligation reaction. One µl of the ligation mixture is used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract (Stratagene, #227711). Phage are plated directly without amplification from the packaging mixture (after dilution with 500 µl of recommended SM buffer and chloroform treatment). Yield is about 2.5x103 pfu/ul. An amplified library is prepared by infecting restructure NM539 host E. coli cells eitn approximately 1x104 phage particles and recovering the progeny phages particles. The recovered phage is stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1x109 pfu/ml.

For high throughput sequencing of individual lambda phage clones, liquid lysates (100 µl) are prepared from randomly selected plaques (from the unamplified library) and template is prepared by long-range PCR using T7 and T3 vector-specific primers.

Sequencing reactions are carried out on plasmid and/or PCR templates using the AB Catalyst LabStation with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers (Adams *et al.*, *Nature 368*:474 (1994)). Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are performed by eight individuals using an average of fourteen AB 373 DNA Sequencers per day. All sequencing reactions are analyzed using the Stretch modification of the AB 373, primarily using a 34 cm well-to-read distance. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

Richards *et al.*, Chapter 28 in AUTOMATED DNA SEQUENCING AND ANALYSIS, M. D. Adams, C. Fields, J. C. Venter, Eds., Academic Press, London, (1994) described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects of lambda and cosmid clones. We balance the desirability of both-end sequencing (including the reduced cost of lower total

number of templates) against shorter read-lengths for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. Approximately one-half of the templates are sequenced from both ends. Random reverse sequencing reactions are done based on successful forward sequencing reactions. Some M13RP1 sequences are obtained in a semi-directed fashion: M13-21: sequences pointing outward at the ends of contigs are chosen for M13RP1 sequencing in an effort to specifically order contigs.

4. Protocol for Automated Cycle Sequencing

The sequencing was carried out using ABI Catalyst robots and AB 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates are combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (*i.e.*., one primer synthesis) steps are performed including denaturation, annealing of primer and template, and extension; *i.e.*, DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols are used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR- generated templates with both dye-primers and dye-terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions are loaded per AB373 Sequencer each day, for a total of 960 samples. Electrophoresis is run overnight following the manufacturer's protocols, and the data is collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking is confirmed visually. Each sequence electropherogram (or fluorescence lane trace) is inspected visually and assessed for quality. Trailing sequences of low quality are removed and the sequence itself is loaded via software to a Sybase database (archived daily to 8mm

tape). Leading vector polylinker sequence is removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 are around 400 bp and depend mostly on the quality of the template used for the sequencing reaction. ABI 373 Sequencers converted to Stretch Liners provide a longer electrophoresis path prior to fluorescence detection and increase the average number of usable bases to 500-600 bp.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen is based on a Unix platform, it was necessary to design and implement a variety of multi- user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments is employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 104 fragments, the algorithm builds a hash table of 10 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology* *164*:765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These

criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library).

The process resulted in 982 contigs as represented by SEQ ID NOs:1-982.

3. Identifying Genes

The predicted coding regions of the *Enterococcus faecalis* genome were initially defined with the program GeneMark, which finds ORFs using a probabilistic classification technique. The predicted coding region sequences were used in searches against a database of all *Enterococcus faecali* nucleotide sequences from GenBank (March, 1997), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases. ORFs that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Enterococcus faecalis* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monocl nal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature 256*:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol. 70*:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al., Basic Methods in Molecular Biology,* Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al., J. Clin.* Endocrinol. Metab. 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology,* Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0. 1 to 0. 2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as

described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, antibodies are useful in various animal models of enterococcal disease as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic or immunoprophylactic reagent.

4. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Enterococcus faecalis* genome, such as those of Tables 1-3 and SEQ ID NOS:1-982 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

5. Isolation of a Selected DNA Clone From the Deposited Sample of E. faecalis

Three approaches can be used to isolate a *E. faecalis* clone comprising a polynucleotide of the present invention from any *E. faecalis* genomic DNA library. The *E. faecalis* strain V586 has been deposited as a convienent source for obtaining a *E. faecalis* strain although a wide varity of strains *E. faecalis* strains can be used which are known in the art.

E. faecalis genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, ished two times with TES (3OmM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear). A CsCl gradient is then set up in

SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *E. faecalis* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (*See, e.g.*, Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. *See, e.g.*, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCALS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. *See, e.g.*, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCALS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of SEQ ID NOS:1-982 are synthesized and used to amplify the desired DNA by PCR using a *E. faecalis* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above DNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the

DNA product.

Finally, overlapping oligos of the DNA sequences of SEQ ID NOS:1-982 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

6(a). Expression and Purification Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 was used for bacterial expression of some of the polypeptide fragements of the present invention which were used in the soft tissue and systemic infection models discussed below. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of a *E. faecalis* protein of the present invention was amplified from *E. faecalis* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *E. faecalis* polynucleotide shown in SEQ ID NOS:1-982. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *E. faecalis* polynucleotide sequence in SEQ ID NOS:1-982. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form. The 3' primer has a sequence containing an appropriate restriction site followed by nucleotides complementary to the 3' end of the polypeptide coding sequence of SEQ ID NOS:1-982, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *E. faecalis* DNA fragment and the vector pQE60 were digested with restriction enzymes which recognize the sites in the primers and the digested DNAs were then ligated together. The *E. faecalis* DNA was inserted into the restricted pQE60

vector in a manner which places the *E. faecalis* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture was transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al., *supra*.. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), was used in carrying out the illustrative example described herein. This strain, which was only one of many that are suitable for expressing a *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants were identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA was isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs were grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 μg/ml) and kanamycin (25 μg/ml). The O/N culture was used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells were grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") was then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently were incubated further for 3 to 4 hours. Cells then were harvested by centrifugation.

The cells were then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris was removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide was loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity were purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the supernatant was loaded onto the column in 6 M guanidine-HCl, pH 8, the column was first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *E. faecalis* polypeptide was eluted with 6 M guanidine-HCl, pH 5.

The purified protein was then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM immidazole. Immidazole was removed by a final dialyzing step against PBS or 50 mM sodium acetate

pH 6 buffer plus 200 mM NaCl. The purified protein was stored at 4° C or frozen at -80° C.

Some of the polypeptide of the present invention were prepared using a non-denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture was resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm was approximately 10-20 O.D./ml. The suspension was then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells were lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample was then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant was passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction was collected.

The pre-cleared flow-through was applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant was loaded onto the column in Lysis Buffer A at 4°C, the column was first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column was washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein was eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations were used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein were analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein was then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein was stored at 4° C or frozen at -80°.

The following alternative method may be used to purify *E. faecalis* expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit

weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x *g* for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x *g* centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x *g*) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 μm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 mm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

6(b). Alternative Expression and Purification Enterococcal polypeptides in E. coli

Tthe vector pQE10 was alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example . The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (*i.e.*, a "6 X His tag")) covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of SEQ ID NOS:1-982 were amplified using PCR oligonucleotide primers from genomic *E. faecalis* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain its reading frame with that of *E. faecalis* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences encoding the amino acid sequences of SEQ ID NOS:1-982 may also be cloned and expressed as fusion proteins by a protocol similar to that described directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragements actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragements therof.

6(c). Alternative Expression and Purification of Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *E. faecalis* amino acid sequence is amplified from an *E. faecalis* genomic DNA prep the deposited DNA clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *E. faecalis* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

For cloning a *E. faecalis* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

The amplified *E. faecalis* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs are then ligated together. Insertion of the *E. faecalis* DNA into the restricted pQE60 vector places the *E. faecalis* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are

identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 μg/ml) and kanamycin (25 μg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *E. faecalis* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. faecalis* polypeptide. The purified protein is stored at 4° C or frozen at -80° C.

The following alternative method may be used to purify *E. faecalis* polypeptides expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells ware then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x *g* for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x *g* centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x *g*) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 mm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

6(d). Cloning and Expression of E. faecalis in Other Bacteria

E. faecalis polypeptides can also be produced in: *E. faecalis* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr.

Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods Chang et al., U.S. Patent No. 4,952,508.

7. Cloning and Expression in COS Cells

A *E. faecalis* expression plasmid is made by cloning a portion of the DNA encoding a *E. faecalis* polypeptide into the expression vector pDNAI/Amp or pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding a *E. faecalis* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *E. faecalis* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *E. faecalis* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *E. faecalis* DNA, a stop codon, and a convenient restriction site.

The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the fragment encoding the *E. faecalis* polypeptide

For expression of a recombinant *E. faecalis* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *E. faecalis* by the vector.

Expression of the *E. faecalis*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ^{35}S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

8. Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *E. faecalis* polypeptide in this example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.*, Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell 41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites

that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human ß-actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLVI. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. faecalis* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *E. faecalis* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *E. faecalis* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five µg of the expression plasmid pC4 is cotransfected with 0.5 µg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml

flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM, 2 μM, 5 μM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200 μM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

9. Quantitative Murine Soft Tissue Infection Model for E. faecalis

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following quantitative murine soft tissue infection model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. *See,e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5 X 10^8 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 with sterilized Cytodex 3 microcarrier beads preswollen in sterile PBS (3g/100ml). Mice are anesthetize briefly until docile, but still mobile and injected with 0.2 ml of the Cytodex 3 bead/bacterial mixture into each animal subcutaneously in the inguinal region. After four days, counting the day of injection as day one, mice are sacrificed and the contents of the abscess is excised and placed in a 15 ml conical tube containing 1.0ml of sterile PBS. The contents of the abscess is then enzymatically treated and plated as follows.

The abscess is first disrupted by vortexing with sterilized glass beads placed in the tubes. 3.0mls of prepared enzyme mixture (1.0ml Collagenase D (4.0 mg/ml), 1.0ml Trypsin (6.0 mg/ml) and 8.0 mls PBS) is then added to each tube followed by a 20 min. incubation at 37C. The solution is then centrifuged and the supernatant drawn off. 0.5 ml dH20 is then added and the tubes are vortexed and then incubated for 10 min. at room temperature. 0.5 ml media is then added and samples are serially diluted and plated onto agar plates, and grown overnight at 37C. Plates with distinct and separate colonies are then counted, compared to positive and negative control samples, and quantified. The

method can be used to identify composition and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

10. Murine Systemic Neutropenic Model for E. faecalis Infection

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following qualitative murine systemic neutropenic model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. *See,e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.
Mice are then injected with 250 - 300 mg/kg cyclophosphamide intraperitonially. Counting the day of C.P. injection as day one, the mice are left untreated for 5 days to begin recovery of PMNL'S.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5 X 10^8 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 in 4% Brewer's yeast in media.
Mice are injected with the bacteria/brewer's yeast challenge intraperitonially. The Brewer's yeast solution alone is used as a control. The mice are then monitered twice daily for the first week following challenge, and once a day for the next week to ascertain morbidity and mortality. Mice remaining at the end of the experiment are sacrificed. The method can be used to identify compositions and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans

and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparant to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
3	2	423	1226	gb|U24692|	"Enterococcus faecalis pyrimidine biosynthesis D (pyrD) gene, complete cds"	99	229
47	14	17085	16216	gb|M81466|	"Enterococcus faecalis RecA protein (recA) gene, partial cds"	98	308
52	1	50	1441	emb|X62755|SFNPRG	S.faecalis npr gene for NADH peroxidase	98	1374
52	2	2456	1494	emb|X62755|SFNPRG	S.faecalis npr gene for NADH peroxidase	100	209
61	1	2	358	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	99	318
61	2	467	1975	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	98	1297
61	3	1749	1967	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	100	136
61	4	1990	2949	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-	100	960

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"		
61	5	2112	2399	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	100	288
61	6	2922	3794	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	100	873
61	7	3671	4762	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	99	1092
61	8	4312	3860	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	100	453
61	9	4653	5783	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB),	100	1131

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"		
61	10	5750	6397	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	99	648
61	11	7158	6784	gb|U35369|	"Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>"	100	161
67	1	3	809	gb|U24692|	"Enterococcus faecalis pyrimidine biosynthesis D (pyrD) gene, complete cds"	98	807
67	2	781	1512	gb|U24692|	"Enterococcus faecalis pyrimidine biosynthesis D (pyrD) gene, complete cds"	93	92
69	1	1	228	gb|U60038|	"Enterococcus faecalis major cold-shock protein (cspA) gene, partial cds"	100	136
72	15	15814	19737	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	92	2504
72	16	19739	20155	emb|X62657|EFORF3	E.faecalis plasmid pAD1 DNA for orf3	96	341
75	1	3	365	emb|Z19137|EFPTSHGN	E.faecalis of ptsH gene encoding HPr	100	267
83	12	8766	7432	emb|X78425|EFPBP5	E.faecalis pbp5 gene	98	416
83	13	8869	9699	emb|X78425|EFPBP5	E.faecalis pbp5 gene	99	819
83	14	9612	10913	emb|X78425|EFPBP5	E.faecalis pbp5 gene	99	1203
83	15	10943	11746	emb|X78425|EFPBP5	E.faecalis pbp5 gene	97	286

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
84	2	1657	3558	emb|X86176|EFRPODDNE	E.faecalis dnaE and rpoD gene	99	797
84	3	3649	4773	emb|X86176|EFRPODDNE	E.faecalis dnaE and rpoD gene	99	1125
84	4	4913	7000	emb|X86176|EFRPODDNE	E.faecalis dnaE and rpoD gene	99	301
104	2	4018	2900	gb|U36195|	"Enterococcus faecalis pyrAa gene, partial cds"	93	310
108	7	5875	5183	gb|M58002|	"Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds"	98	252
145	8	8193	7234	gb|U03756|	"Enterococcus faecalis endocarditis specific antigen gene, complete cds"	99	960
145	9	8836	8147	gb|U03756|	"Enterococcus faecalis endocarditis specific antigen gene, complete cds"	100	132
147	3	2096	3418	emb|X68847|SFNOXAA	S.faecalis nox gene for NADH oxidase	99	1301
154	4	2160	2492	emb|X17092|PPRRA	Plasmid pAM-beta-1 (from S.faecalis) replication region DNA	93	294
154	10	5935	6294	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	99	355
154	11	6279	6584	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	98	89
154	12	7882	7097	gb|U86375|	"Enterococcus faecalis ermB regulator and adenine methylase (ermB) genes, complete cds"	99	736
154	13	8750	8043	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	99	498
159	1	158	1483	gb|M58002|	"Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds"	98	1323
159	2	807	157	gb|M58002|	"Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds"	99	651
159	3	1395	2192	gb|M58002|	"Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds"	93	350

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
216	2	282	1841	gb|M90060|	"Streptococcus faecalis H+ ATPase a (atpB),b (atpF),c (atpE),alpha (atpA), beta (atpD),gamma (atpG),delta (atpH),and epsilon (atpC) subunits, complete cds"	81	1558
216	4	2809	2967	gb|M90060|	"Streptococcus faecalis H+ ATPase a (atpB),b (atpF),c (atpE),alpha (atpA), beta (atpD),gamma (atpG),delta (atpH),and epsilon (atpC) subunits, complete cds"	86	132
216	5	2940	4244	gb|M90060|	"Streptococcus faecalis H+ ATPase a (atpB),b (atpF),c (atpE),alpha (atpA), beta (atpD),gamma (atpG),delta (atpH),and epsilon (atpC) subunits, complete cds"	83	1293
238	3	1814	2218	gb|M38386|	"Streptococcus faecalis mtlF enzymeIII, mannitol-mtlD-phosphate- dehydrogenase"	96	302
238	4	2182	2670	gb|M38386|	"Streptococcus faecalis mtlF enzymeIII, mannitol-mtlD-phosphate- dehydrogenase"	98	480
238	5	2634	3839	gb|M38386|	"Streptococcus faecalis mtlF enzymeIII, mannitol-mtlD-phosphate- dehydrogenase"	96	459
261	2	1397	510	emb|Z12296|EFSPREG	E.faecalis sprE gene for serine proteinase homologue	98	888
261	3	2474	1413	dbj|D85393|ENEGE1E	"Enterococcus faecalis DNA for gelatinase, complete cds"	98	1051
261	4	2974	2417	dbj|D85393|ENEGE1E	"Enterococcus faecalis DNA for gelatinase, complete cds"	97	516
275	3	1472	1044	gb|L23802|	"Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region"	98	422
275	4	1581	2018	gb|L23802|	"Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins	97	438

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					(ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region"		
275	5	2789	2148	gb|L23802|	"Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region"	98	642
275	6	3475	2660	gb|L23802|	"Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region"	98	790
287	2	1565	558	emb|X17092|PPRRA	Plasmid pAM-beta-1 (from S.faecalis) replication region DNA	97	991
287	3	2049	1582	emb|X17092|PPRRA	Plasmid pAM-beta-1 (from S.faecalis) replication region DNA	97	461
287	6	2639	3346	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	99	498
294	11	4519	4211	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	100	50
302	1	1	1755	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	83	1755
302	2	2310	2687	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	100	378
302	3	2865	3329	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	99	463
316	4	2724	2110	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	100	248
346	5	2224	2880	emb|X62755|SFNPRG	S.faecalis npr gene for NADH peroxidase	98	351

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
349	2	686	907	dbj|D78257|D78257	"Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds"	83	200
355	1	3	1166	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	97	1100
355	2	1102	1548	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	94	432
355	3	1663	2037	emb|X62657|EFORF3	E.faecalis plasmid pAD1 DNA for orf3	99	337
355	4	2035	2445	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	99	411
355	5	2558	2851	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	96	280
355	6	2838	3299	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	97	430
355	7	3236	3739	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	97	279
355	8	3696	4529	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	97	537
355	9	4587	5870	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	98	718
355	10	5843	6490	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	99	224
355	11	6471	6890	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	96	361
355	12	6881	7204	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	98	324
355	13	7191	8231	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	98	984
355	14	8218	8496	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	99	279
355	15	8412	8885	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading	100	474

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					frames"		
355	17	9479	9952	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	98	417
365	1	3	380	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	100	248
370	1	1	1299	dbj|D78016|ENEPPD1A	"Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds"	73	1267
407	3	963	2162	gb|U38590|	"Enterococcus faecalis plasmid pCF10 PrgN, PrgO, and PrgP genes, complete cds"	98	257
407	5	3811	4131	gb|U38590|	"Enterococcus faecalis plasmid pCF10 PrgN, PrgO, and PrgP genes, complete cds"	86	317
417	1	42	419	gb|U00681|	"Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds"	98	304
417	2	313	41	gb|U00681|	"Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds"	97	198
417	3	440	754	gb|U00681|	"Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds"	100	219
426	1	112	462	emb|Z49243|EF4110SOD	E.faecalis partial sod gene for superoxide dismutase (strain=BM4110)	98	291
426	2	628	419	emb|Z49243|EF4110SOD	E.faecalis partial sod gene for superoxide dismutase (strain=BM4110)	100	148
426	3	456	725	emb|Z49243|EF4110SOD	E.faecalis partial sod gene for superoxide dismutase (strain=BM4110)	100	148
429	1	840	79	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	98	737
429	2	1087	767	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	99	321
429	4	2765	2460	gb|U17153|	"Enterococcus faecalis plasmid pjh1	98	89

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					tetracycline resistant (tetL) gene, complete cds"		
429	5	3166	2750	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	99	413
435	5	2731	2324	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	97	97
459	2	1330	1067	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	99	248
506	1	1242	4	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	99	1144
514	3	1496	1113	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	100	248
527	2	1733	1371	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	98	153
544	1	309	4	gb|U38590|	"Enterococcus faecalis plasmid pCF10 PrgN, PrgO, and PrgP genes, complete cds"	95	306
561	1	3	761	dbj|D78016|ENEPPD1A	"Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds"	77	528
561	2	772	1566	gb|U00681|	"Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds"	99	795
566	3	874	2037	dbj|D78016|ENEPPD1A	"Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds"	90	1160
581	1	398	3	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading	100	393

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					frames"		
581	2	908	540	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	100	369
597	1	573	7	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	99	566
597	2	1247	516	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	97	701
604	7	3265	2903	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	100	143
618	1	1	534	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	99	470
622	1	864	16	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	99	849
622	2	1317	862	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	99	256
622	3	1586	1311	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	99	248
624	6	5641	8001	gb|U66286|	"Enterococcus faecalis gyrase A (gyrA) gene, partial cds"	98	219
635	1	516	953	dbj|D78257|D78257	"Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds"	94	404

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
635	2	920	1222	dbj|D78257|D78257	"Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds"	83	299
637	1	3	545	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	92	506
658	2	1198	365	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	100	819
658	3	1446	1189	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	98	258
664	1	490	65	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	88	423
664	2	737	417	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	94	321
743	1	561	4	dbj|D78016|ENEPPD1A	"Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds"	87	305
747	2	1139	324	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	99	691
747	3	577	783	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	100	207
747	4	1474	1133	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	99	248
777	1	401	3	gb|M38052|	"Enterococcus faecalis cytolysin B transport protein gene, complete cds"	100	335
816	1	793	512	gb|M13771|	"Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds"	100	243
842	1	418	89	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	91	303
842	2	856	605	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	92	246

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
847	1	1481	3	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	92	1479
864	1	36	1106	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	93	945
864	2	1571	3550	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	96	1979
872	1	263	3	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	98	261
874	1	833	693	dbj|D31675|ENE16RNA8	"Enterococcus faecalis 16S ribosomal RNA, partial sequence"	100	98
878	1	302	30	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	94	94
878	2	263	445	gb|U17153|	"Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds"	99	181
921	1	748	26	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	95	612
929	1	484	2	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	99	409
946	1	3	422	emb|X62657|EFORF3	E.faecalis plasmid pAD1 DNA for orf3	99	341
946	2	420	830	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	98	411
946	3	866	1123	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	96	230
947	1	112	498	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	96	378
951	1	484	26	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	95	353
956	1	3	545	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	96	543
956	2	524	721	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	94	161
957	1	616	2	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading frames"	99	615
957	2	42	686	emb|X96977|EFPAD1ORF	"E.faecalis plasmid pAD1, open reading	99	595

Table 1: *E. faecalis* - Coding regions containing known sequences

Contig ID	Orf ID	Start (nt)	Stop (nt)	Match Accession	Match Gene Name	Percent Indent	HSP nt length
					frames"		
968	1	1	456	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	96	366
968	2	339	641	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	95	158
968	3	395	658	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	94	126
977	1	5	943	emb|X17214|SFPASA1	S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1	99	847
982	1	376	2	emb|X62658|EFSEA1	E.faecalis plasmid pAD1 sea1 gene and orfy	95	365
985	1	85	471	emb|X62656|EFASP1	"E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes"	91	362

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
137	3	3208	2003	gi|152947	transposase [Staphylococcus aureus]	100	100
154	14	9166	9750	gi|141861	traA gene product [Plasmid pAD1]	100	100
276	16	11268	11047	gnl|PID|e284733	C34B7.2 [Caenorhabditis elegans]	100	71
287	1	485	234	gi|152947	transposase [Staphylococcus aureus]	100	100
287	7	3454	3765	gi|152947	transposase [Staphylococcus aureus]	100	100
292	6	3001	4185	gi|488330	alpha-amylase [unidentified cloning vector]	100	100
429	3	2013	1654	gi|141863	regulatory protein [Plasmid pAD1]	100	100
604	3	1243	1043	gi|559860	clyLs [Plasmid pAD1]	100	98
604	4	1492	1268	gi|559859	clyLl [Plasmid pAD1]	100	100
656	7	7592	6834	gi|488339	alpha-amylase [unidentified cloning vector]	100	100
658	1	312	4	gi|152947	transposase [Staphylococcus aureus]	100	100
674	3	1236	1589	gi|1196996	unknown protein [Transposon Tn10]	100	98
700	1	375	4	gi|152947	transposase [Staphylococcus aureus]	100	100
961	1	1	450	gi|152947	transposase [Staphylococcus aureus]	100	100
72	17	20153	21040	gi|150556	surface protein [Plasmid pCF10]	99	99
99	5	3117	1933	gi|1006839	malic enzyme [Streptococcus bovis]	99	99
154	3	1955	1491	gi|149482	transposase [Lactococcus lactis]	99	99
326	3	3030	1774	pir|S16989|S16989	dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Enterococcus faecalis	99	98
407	6	4636	4235	gi|141859	replication-associated protein [Plasmid pAD1]	99	99
692	1	3	485	gi|559861	clyM [Plasmid pAD1]	99	99
99	6	3904	3134	gi|1146122	L-malate permease [Streptococcus bovis]	98	98
326	4	3358	3002	pir|S16989|S16989	dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Enterococcus faecalis	98	97
346	1	606	4	gi|1146122	L-malate permease [Streptococcus bovis]	98	98
367	31	14415	13999	gi|1644226	ribosomal protein S10 [Bacillus subtilis]	98	88
367	6	2797	2495	gi|142459	initiation factor 1 [Bacillus subtilis]	97	88
407	9	5454	4894	gi|141858	replication-associated protein [Plasmid	97	97

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					pAD1]		
497	6	3514	3762	gi|532552	ORF19 [Enterococcus faecalis]	97	87
558	1	1	399	gi|46638	ORF 2 (AA 1 - 236) [Staphylococcus aureus]	97	97
829	1	169	2	gnl|PID|e283110	femD [Staphylococcus aureus]	97	86
407	8	4970	4599	gi|141858	replication-associated protein [Plasmid pAD1]	96	96
777	2	1102	380	gi|559861	clyM [Plasmid pAD1]	96	96
23	33	20797	21126	gnl|PID|e223402	DNA topoisomerase IV C subunit [Streptococcus pneumoniae]	95	80
32	5	3454	3071	gi|147194	phnA protein [Escherichia coli]	95	87
95	8	5493	6875	gi|391682	Na+ -ATPase beta subunit [Enterococcus hirae]	95	89
138	25	16587	16745	gi|143136	L-lactate dehydrogenase [Bacillus megaterium]	95	70
367	20	9198	8797	gi|40150	L14 protein (AA 1-122) [Bacillus subtilis]	95	90
367	21	9519	9223	gi|1044973	ribosomal protein L17 [Bacillus subtilis]	95	89
439	2	846	1241	gi|488334	alpha-amylase [unidentified cloning vector]	95	94
604	1	792	4	gi|559861	clyM [Plasmid pAD1]	95	93
722	1	1	504	gi|47453	ribosomal protein S12 [Streptococcus pneumoniae]	95	94
17	8	7317	7676	gi|532554	ORF21 [Enterococcus faecalis]	94	86
95	2	1288	1791	gi|416405	Na+-ATPase K subunit [Enterococcus hirae]	94	88
97	3	2481	1432	gi|1750264	heat shock protein 70 [Streptococcus pneumoniae]	94	90
117	5	2700	3842	gi|467376	unknown [Bacillus subtilis]	94	89
327	3	3283	3762	gi|153566	ORF (19K protein) [Enterococcus faecalis]	94	87
327	5	4782	5054	gi|153568	H+ ATPase [Enterococcus faecalis]	94	82
387	4	3608	1728	gi|153661	translational initiation factor IF2 [Enterococcus faecium] sp|P18311|IF2_ENTFC INITIATION FACTOR IF-2.	94	88

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
455	1	2	259	gi|532549	ORF16 [Enterococcus faecalis]	94	82
97	2	1444	677	gi|450684	dnaK gene product [Lactococcus lactis]	93	83
188	2	1690	1911	gi|43865	nifJ gene product [Klebsiella pneumoniae]	93	78
216	6	4234	4680	gi|153574	H+ ATPase [Enterococcus faecalis]	93	86
298	2	2798	1221	gi|143012	GMP synthetase [Bacillus subtilis]	93	86
329	2	1538	771	gi|153826	adhesin B [Streptococcus sanguis]	93	83
367	15	7675	7247	gi|1044978	ribosomal protein S8 [Bacillus subtilis]	93	82
722	2	527	1030	gi|1644222	ribosomal protein S7 [Bacillus subtilis]	93	83
803	1	657	151	gi|1196998	unknown protein [Transposon Tn10]	93	93
962	1	130	636	gi|152947	transposase [Staphylococcus aureus]	93	92
237	12	6056	6385	gi|963038	ArpU [Enterococcus hirae]	92	76
309	4	8218	4541	gi|402363	RNA polymerase beta-subunit [Bacillus subtilis] sp|P37870|RPOB_BACSU DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC .7.7.6) (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).	92	82
329	4	2529	1717	gi|310632	hydrophobic membrane protein [Streptococcus gordonii] sp|P42361|P29K_STRGC 29 KD MEMBRANE PROTEIN IN PSAA 5'REGION ORF1).	92	78
367	4	1942	1544	gi|142462	ribosomal protein S11 [Bacillus subtilis]	92	82
367	8	3648	3457	pir|C44859|C44859	adenylate kinase - Bacillus sp. (fragment)	92	88
367	12	6183	5641	gi|1044981	ribosomal protein S5 [Bacillus subtilis]	92	81
367	17	8427	7885	pir|A29102|R5BS5F	ribosomal protein L5 - Bacillus stearothermophilus	92	83
527	1	1404	373	gi|153092	replication protein [Staphylococcus aureus]	92	81
701	1	2	352	gi|143793	tyrosyl-tRNA synthetase [Bacillus caldotenax]	92	74
23	28	17420	17566	sp|P45692|EUTX_SALTY	ETHANOLAMINE UTILIZATION PROTEIN EUTX (FRAGMENT).	91	73

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
57	5	4129	4701	gi|1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	91	67
57	12	13281	13970	gnl|PID|e254999	phenylalany-tRNA synthetase beta subunit [Bacillus subtilis]	91	75
156	5	4609	6474	gi|1303804	YqeQ [Bacillus subtilis]	91	79
216	3	1848	2765	gi|153572	H+ ATPase [Enterococcus faecalis]	91	81
367	24	10802	10128	gi|1165309	S3 [Bacillus subtilis]	91	78
415	1	452	883	pir|B56272|B56272	probable pheromone-responsive regulatory protein R - Enterococcus faecalis plasmid pCF10	91	90
466	2	1313	2065	gi|142443	adenylosuccinate synthetase [Bacillus subtilis] sp|P29726|PURA_BACSU ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) IMP--ASPARTATE LIGASE).	91	79
545	1	1	345	gi|532549	ORF16 [Enterococcus faecalis]	91	80
572	1	8	652	gi|347998	uracil phosphoribosyltransferase [Streptococcus salivarius] sp|P36399|UPP_STRSL PROBABLE URACIL PHOSPHORIBOSYLTRANSFERASE (EC .4.2.9) (UMP PYROPHOSPHORYLASE) (UPRTASE).	91	78
599	1	8	343	gi|42029	ORF1 gene product [Escherichia coli]	91	75
600	2	585	779	pir|B48396|B48396	ribosomal protein L33 - Bacillus stearothermophilus	91	81
652	1	394	2	gi|535662	transposase [Insertion sequence IS1251]	91	81
1	4	3465	2557	gi|1644224	elongation factor Tu [Bacillus subtilis]	90	83
17	19	14844	17297	gi|532549	ORF16 [Enterococcus faecalis]	90	77
52	3	2650	2811	gi|473902	alpha-acetolactate synthase [Lactococcus lactis]	90	68
74	9	5870	5469	gi|1653508	hypothetical protein [Synechocystis sp.]	90	52
75	3	1177	2091	gi|153615	phosphoenolpyruvate:sugar phosphotransferase system enzyme I Streptococcus salivarius]	90	83

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
117	10	6591	8126	gi|924848	inosine monophosphate dehydrogenase [Streptococcus pyogenes] pir|JC4372|JC4372 IMP dehydrogenase (EC 1.1.1.205) - Streptococcus yogenes	90	80
276	1	577	95	gi|530798	LysB [Bacteriophage phi-LC3]	90	72
287	5	2611	2441	gi|1333835	copS gene product [Streptococcus pyogenes]	90	78
290	1	1	708	gi|897795	30S ribosomal protein [Pediococcus acidilactici] sp|P49668|RS2_PEDAC 30S RIBOSOMAL PROTEIN S2.	90	75
309	3	4401	1093	gnl|PID|e187579	DNA-directed RNA polymerase [Listeria innocua]	90	81
367	22	9731	9513	pir|A02825|R5BS29	ribosomal protein L29 - Bacillus stearothermophilus	90	76
452	4	2224	2508	gi|434759	ORF [Homo sapiens]	90	54
455	2	2776	323	gi|532549	ORF16 [Enterococcus faecalis]	90	77
623	1	3	221	gi|460259	enolase [Bacillus subtilis]	90	80
624	5	3612	5615	gnl|PID|e208213	DNA gyrase [Streptococcus pneumoniae]	90	81
853	2	752	282	gnl|PID|e13389	translation initiation factor IF3 (AA 1-172) [Bacillus stearothermophilus]	90	82
966	1	1	462	gi|532549	ORF16 [Enterococcus faecalis]	90	83
1	3	2596	2219	gi|1661195	elongation factor-Tu [Streptococcus mutans]	89	78
1	5	4314	3556	gi|1644223	elongation factor G [Bacillus subtilis]	89	79
23	21	13990	14295	gi|466518	pduA [Salmonella typhimurium]	89	75
23	32	19927	20799	gnl|PID|e208211	DNA topoisomerase IV [Streptococcus pneumoniae]	89	83
42	2	349	1989	gi|287871	groEL gene product [Lactococcus lactis]	89	79
45	15	11835	12167	gi|150554	surface exclusion protein [Plasmid pCF10]	89	68
53	2	685	1797	gnl|PID|e221213	ClpX protein [Bacillus subtilis]	89	81
86	4	3374	4024	gi|537286	triosephosphate isomerase [Lactococcus lactis]	89	78

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
95	7	3677	5506	gi|912449	Na+ -ATPase alpha subunit [Enterococcus hirae]	89	80
128	18	11348	11013	gi|466473	cellobiose phosphotransferase enzyme II' [Bacillus tearothermophilus]	89	60
132	1	180	2180	gi|153854	uvs402 protein [Streptococcus pneumoniae]	89	78
342	1	783	4	gi|1041115	TRAC [Plasmid pPD1]	89	79
367	23	10146	9691	sp|P14577|RL16_BACSU	50S RIBOSOMAL PROTEIN L16.	89	80
367	27	12377	11541	gi|1165306	L2 [Bacillus subtilis]	89	79
435	4	2424	2215	gi|559863	clyA [Plasmid pAD1]	89	89
466	3	1972	2736	gi|467328	adenylosuccinate synthetase [Bacillus subtilis]	89	75
512	3	999	1607	gi|1477776	ClpP [Bacillus subtilis]	89	73
518	1	1	174	gi|786163	Ribosomal Protein L10 [Bacillus subtilis]	89	76
604	2	1000	713	gi|559861	clyM [Plasmid pAD1]	89	89
615	2	888	691	gi|467469	unknown [Bacillus subtilis]	89	75
677	2	992	429	gi|1389732	S-adenosylmethionine synthetase [Bacillus subtilis]	89	76
677	3	1315	950	gi|1020317	S-adenosylmethionine synthetase [Staphylococcus aureus]	89	73
722	3	1102	1278	pir|PW0010|PW0010	translation elongation factor G - Bacillus stearothermophilus (fragment)	89	72
850	1	464	3	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] gnl|PID|e255102 deoxyribodipyrimidine photolyase [Bacillus ubtilis]	89	72
17	5	3711	4751	gi|532554	ORF21 [Enterococcus faecalis]	88	72
37	5	3322	3717	gi|1216488	uncharacterized open reading frame; hypothetical protein displaying similarity to a Bacillus subtilis hypothetical protein (Ylm [Streptococcus mutans]	88	75
39	6	2454	2630	sp|P49865|NTPR_ENT	NTPR PROTEIN (FRAGMENT).	88	77

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
				HR			
48	3	1740	2666	gi|557492	dihydroxynapthoic acid (DHNA) synthetase [Bacillus subtilis] gi|143186 dihydroxynapthoic acid (DHNA) synthetase [Bacillus ubtilis]	88	75
63	5	2753	3607	gi|1064814	homologous to sp:PHOP_BACSUB [Bacillus subtilis]	88	77
86	2	1004	2047	gi|153763	plasmin receptor [Streptococcus pyogenes]	88	79
104	6	6431	6213	gi|431231	uracil permease [Bacillus caldolyticus]	88	60
110	19	18174	16891	gi|217040	acid glycoprotein [Streptococcus pyogenes]	88	72
145	10	9040	8834	gi|393268	29-kiloDalton protein [Streptococcus pneumoniae] sp|P42362|P29K_STRPN 29 KD MEMBRANE PROTEIN IN PSAA 5'REGION ORF1).	88	71
151	1	1620	316	gi|143366	adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis	88	78
171	10	9676	10119	gi|1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	88	63
190	3	1997	975	gi|532554	ORF21 [Enterococcus faecalis]	88	76
229	6	5712	5954	gi|143648	ribosomal protein L28 [Bacillus subtilis]	88	70
270	2	895	1869	gi|1303828	YqfJ [Bacillus subtilis]	88	75
275	7	3761	3552	gi|425474	SMDR1 [Schistosoma mansoni]	88	72
293	1	614	3	gi|1783246	highly homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis]	88	80
367	1	485	72	gi|142464	ribosomal protein L17 [Bacillus subtilis]	88	76
367	5	2335	1961	gi|1044989	ribosomal protein S13 [Bacillus subtilis]	88	80
367	16	7887	7681	pir|S48688|S48688	ribosomal protein S14 - Bacillus stearothermophilus	88	83
598	1	1006	23	gi|565287	transposase-like protein of PS3IS [thermophilic bacterium PS3]	88	66

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					pir|JC4292|JC4292 insertion sequence element 1341 - thermophilic acterium PS-3		
600	3	1640	882	gi|763052	integrase [Bacteriophage T270]	88	68
669	1	2	514	gi|153801	enzyme scr-II [Streptococcus mutans]	88	75
808	2	624	394	gi|1574781	exodeoxyribonuclease V (recB) [Haemophilus influenzae]	88	77
871	1	714	229	gi|1574120	branched-chain-amino-acid transaminase [Haemophilus influenzae]	88	79
979	1	1	384	gnl|PID|e187579	DNA-directed RNA polymerase [Listeria innocua]	88	78
983	1	34	282	gi|40026	homologous to E.coli gidA [Bacillus subtilis]	88	78
47	5	6799	5810	gi|532204	prs [Listeria monocytogenes]	87	79
69	3	2033	750	gi|1377831	unknown [Bacillus subtilis]	87	74
73	2	1432	167	gi|143434	Rho Factor [Bacillus subtilis]	87	76
76	5	2412	3740	gi|496283	lysin [Bacteriophage Tuc2009]	87	75
88	3	1600	2016	gnl|PID|e137596	heat shock induced protein HtpO [Lactobacillus leichmannii]	87	75
89	7	6003	5608	gi|1695686	pyruvate carboxylase [Bacillus stearothermophilus]	87	77
93	1	283	119	gi|1124825	unknown protein [Chlamydia trachomatis]	87	56
104	1	2945	3	gnl|PID|e199387	carbamoyl-phosphate synthase [Lactobacillus plantarum]	87	75
124	4	3191	2274	gi|995767	UDP-glucose pyrophosphorylase [Streptococcus pyogenes]	87	76
273	2	608	1108	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	87	76
293	2	1020	532	gi|153741	ATP-binding protein [Streptococcus mutans]	87	74
326	5	4534	3533	gi|143378	pyruvate decarboxylase (E-1) beta subunit [Bacillus subtilis] gi|1377836 pyruvate decarboxylase E-1 beta subunit [Bacillus ubtilis]	87	74

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
334	3	3182	3340	pir|A36324|A36324	growth arrest-specific protein - mouse	87	50
337	1	1382	186	gi|308861	GTG start codon [Lactococcus lactis]	87	75
338	8	6925	5723	gi|149575	L(+)-lactate dehydrogenase [Lactobacillus casei] sp|P00343|LDH_LACCA L-LACTATE DEHYDROGENASE (EC 1.1.1.27). (SUB -326)	87	73
367	18	8782	8450	pir|A02819|R5BS24	ribosomal protein L24 - Bacillus stearothermophilus	87	70
388	2	410	183	gnl|PID|e225674	unknown [Schizosaccharomyces pombe]	87	75
440	1	466	1797	gi|520754	putative [Bacillus subtilis]	87	75
508	1	694	137	gi|496558	orfX [Bacillus subtilis]	87	73
654	3	530	802	pir|A47079|A47079	heat shock protein DnaJ - Lactococcus lactis	87	70
18	1	3	413	gi|46912	ribosomal protein L13 [Staphylococcus carnosus]	86	70
18	2	406	819	pir|S08564|R3BS9	ribosomal protein S9 - Bacillus stearothermophilus	86	73
50	1	84	1148	gi|452398	threonine synthase [Bacillus sp.]	86	74
74	14	10547	10080	gi|1314299	ORF6; putative glutamyl-tRNA-transferase; similar to glutamyl-tRNA-transferase from Bacillus subtilis [Listeria monocytogenes]	86	74
95	5	3176	3406	gi|487276	Na+ -ATPase subunit C [Enterococcus hirae]	86	62
114	8	9216	10313	gi|853776	peptide chain release factor 1 [Bacillus subtilis] pir|S55437|S55437 peptide chain release factor 1 - Bacillus ubtilis	86	69
115	2	501	899	gi|551879	ORF 1 [Lactococcus lactis]	86	70
164	26	25639	25842	pir|S34762|S34762	L-serine dehydratase beta chain - Clostridium sp.	86	81
243	2	2143	1082	gi|143607	sporulation protein [Bacillus subtilis]	86	70
255	1	2	196	gi|755604	unknown [Bacillus subtilis]	86	64
257	3	3565	983	gi|928832	ORF259; putative [Lactococcus lactis phage BK5-T]	86	66

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
273	3	943	1314	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	86	65
288	2	554	1087	gi|153033	tagatose 6-phosphate isomerase [Staphylococcus aureus] pir|B38158|B38158 galactose-6-phosphate isomerase 19K chain - taphylococcus aureus	86	74
327	7	5183	5722	gi|153569	H+ ATPase [Enterococcus faecalis]	86	71
345	7	5111	5620	gi|1314294	ORF1; putative 17 kDa protein [Listeria monocytogenes]	86	63
350	3	1900	2781	gi|511015	dihydroorotate dehydrogenase A [Lactococcus lactis] sp|P54321|PYDA_LACLC DIHYDROOROTATE DEHYDROGENASE A (EC 1.3.3.1) DIHYDROOROTATE OXIDASE A) (DHODEHASE A).	86	73
363	3	3328	4233	gi|1657517	hypothetical protein [Escherichia coli]	86	59
367	25	11216	10851	gi|1165308	L22 [Bacillus subtilis]	86	68
367	26	11534	11220	gi|1165307	S19 [Bacillus subtilis]	86	77
367	30	13995	13453	gi|1165303	L3 [Bacillus subtilis]	86	75
393	1	1	660	sp|P33898|G3P3_ECOLI	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE C (EC 1.2.1.12) (GAPDH-C).	86	77
396	1	1	192	gi|944942	RipX [Bacillus subtilis]	86	77
438	3	1279	1560	gi|1001878	CspL protein [Listeria monocytogenes]	86	75
510	1	1008	199	gi|473795	'ORF' [Escherichia coli]	86	71
510	2	1912	962	gi|473794	'ORF' [Escherichia coli]	86	76
539	1	705	4	gi|467477	unknown [Bacillus subtilis]	86	79
570	2	2069	1023	gi|881511	Ccpa protein [Lactobacillus casei]	86	72
654	2	240	575	pir|A47079|A47079	heat shock protein DnaJ - Lactococcus lactis	86	77
677	1	431	102	gi|1389732	S-adenosylmethionine synthetase [Bacillus subtilis]	86	80
984	1	1	147	pir|A56922|A56922	transcription factor shn - fruit fly (Drosophila melanogaster)	86	73

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
5	11	7720	8487	gi|41015	aspartate-tRNA ligase [Escherichia coli]	85	71
34	2	2133	1711	gi|47828	pyruvate kinase [Bacillus stearothermophilus]	85	75
97	4	2666	2517	pir|S39341|S39341	grpE protein - Lactococcus lactis	85	66
103	2	1263	946	gi|143364	phosphoribosyl aminoimidazole carboxylase I (PUR-E) [Bacillus ubtilis]	85	68
103	3	1465	1169	gi|143364	phosphoribosyl aminoimidazole carboxylase I (PUR-E) [Bacillus ubtilis]	85	67
129	3	2395	3258	gi|143766	(thrSv) (EC 6.1.1.3) [Bacillus subtilis]	85	67
129	4	3240	4445	gi|143766	(thrSv) (EC 6.1.1.3) [Bacillus subtilis]	85	78
188	1	86	1447	gnl|PID|e214721	glutamine synthetase [Staphylococcus aureus]	85	71
217	3	673	1086	gi|520540	unknown [Bacillus subtilis]	85	72
241	2	1715	1086	gi|495089	recombinase [Staphylococcus aureus]	85	68
285	2	712	993	gi|40014	pot. ORF 446 (aa 1-446) [Bacillus subtilis]	85	77
293	3	1149	1595	gi|755604	unknown [Bacillus subtilis]	85	66
300	2	2738	2220	gi|289261	comE ORF2 [Bacillus subtilis]	85	72
305	2	1853	2695	pir|S09411|S09411	spoIIIE protein - Bacillus subtilis	85	70
322	1	1	171	gi|153562	aspartate beta-semialdehyde dehydrogenase (EC 1.2.1.11) Streptococcus mutans]	85	67
327	4	4056	4784	gi|153567	H+ ATPase [Enterococcus faecalis]	85	66
367	10	5417	4959	pir|A02795|R5BS15	ribosomal protein L15 - Bacillus stearothermophilus	85	76
383	3	3168	2953	gnl|PID|e274577	csp [Lactobacillus plantarum]	85	79
404	3	3069	2101	gi|143402	recombination protein (ttg start codon) [Bacillus subtilis] gi|1303923 RecN [Bacillus subtilis]	85	72
469	1	2	724	gi|508979	GTP-binding protein [Bacillus subtilis]	85	78
488	1	1	996	gi|532548	ORF15 [Enterococcus faecalis]	85	67
535	5	6468	4849	gi|634107	kdpB [Escherichia coli]	85	68

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
584	3	732	562	gi|467374	single strand DNA binding protein [Bacillus subtilis] sp|P37455|SSB_BACSU SINGLE-STRAND BINDING PROTEIN (SSB) HELIX-DESTABILIZING PROTEIN).	85	75
695	1	78	500	gi|499384	orf189 [Bacillus subtilis]	85	75
836	1	1	357	gi|153801	enzyme scr-II [Streptococcus mutans]	85	69
17	20	17212	18813	gi|532548	ORF15 [Enterococcus faecalis]	84	68
23	31	18728	19987	gnl|PID|e208211	DNA topoisomerase IV [Streptococcus pneumoniae]	84	68
34	3	3112	2144	gi|143312	6-phospho-1-fructokinase (gtg start codon; EC 2.7.1.11) [Bacillus tearothermophilus]	84	69
36	1	1	1152	gi|1644223	elongation factor G [Bacillus subtilis]	84	73
49	12	6730	8190	gi|456319	74kDa protein [Bacteriophage FC1]	84	65
51	2	1379	1663	gi|468207	Submitter comments: A Mg2+ transporting P-type ATPase highly omologous with mgtB ATPase at 80 min on Salmonella chromosome. ediates the influx of Mg2+ only. Transcription regulated by xtracellular Mg2+ [Salmonella typhimurium]	84	71
95	6	3330	3707	gi|487277	Na+ -ATPase subunit G [Enterococcus hirae]	84	64
104	5	6250	5459	gnl|PID|e199440	aspartate carbamoyltransferase, aspartate transcarbamylase, carbamylaspartotranskinase [Lactobacillus plantarum]	84	65
105	6	4605	5273	gi|467411	recombination protein [Bacillus subtilis]	84	65
114	11	12278	12997	gi|556886	serine hydroxymethyltransferase [Bacillus subtilis] pir|S49363|S49363 serine hydroxymethyltransferase - Bacillus ubtilis	84	74
117	2	705	1484	gi|580906	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis] gi|467381 regulation of Spo0J and Orf283 (probable)	84	70

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Bacillus ubtilis]		
121	2	1274	2119	gi|290643	ATPase [Enterococcus hirae]	84	67
121	6	5016	5219	gi|153765	DNA polymerase I [Streptococcus pneumoniae]	84	66
128	27	22456	20453	gi|437916	isoleucyl-tRNA synthetase [Staphylococcus aureus]	84	71
130	1	2	133	gi|1237013	ORF2 [Bacillus subtilis]	84	74
138	35	26712	25777	gi|143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	84	69
164	28	26378	27277	gnl|PID|e247026	orf6 [Lactobacillus sake]	84	72
171	1	158	2719	gi|499335	secA protein [Staphylococcus carnosus]	84	68
210	5	4870	3884	gi|950062	hypothetical yeast protein 1 [Mycoplasma capricolum] pir|S48578|S48578 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	84	75
217	7	5222	3546	gi|143597	CTP synthetase [Bacillus subtilis]	84	68
243	1	1088	126	gi|143608	sporulation protein [Bacillus subtilis]	84	70
275	1	578	48	gi|1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	84	72
281	1	333	698	gi|1303962	YqjK [Bacillus subtilis]	84	68
292	23	18340	18038	gi|142988	membrane transport protein [Bacillus stearothermophilus] pir|A42478|A42478 glutamine transport protein glnQ - Bacillus tearothermophilus	84	61
309	2	1114	722	gi|1644219	RNA polymerase beta' subunit [Bacillus subtilis]	84	72
315	1	668	3	gi|149601	thymidylate synthase (EC 2.1.1.45) [Lactobacillus casei]	84	72
334	6	5375	6862	gi|1354211	PET112-like protein [Bacillus subtilis]	84	71
338	10	7585	10479	gi|467444	transcription-repair coupling factor [Bacillus subtilis] sp|P37474|MFD_BACSU TRANSCRIPTION-REPAIR COUPLING FACTOR	84	68

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					(TRCF).		
338	14	12713	13018	gi|467448	unknown [Bacillus subtilis]	84	64
340	3	1068	2273	gi|40046	phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus] ir|S15936|NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	84	69
375	2	1430	1780	gi|1402531	ORF10 [Enterococcus faecalis]	84	64
381	1	2	1279	gnl|PID|e208212	DNA topoisomerase IV [Streptococcus pneumoniae]	84	67
421	1	5	151	gi|710632	beta-glucosidase [Bacillus subtilis]	84	73
421	3	1229	1465	gi|710632	beta-glucosidase [Bacillus subtilis]	84	65
445	1	1080	190	gi|46985	glucose-1-phosphate thymidylyltransferase [Salmonella enterica] ir|S23342|S23342 hypothetical protein 6.1 - Salmonella choleraesuis p|P55254|RFBA_SALAN GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 7.7.24) (DTDP-GLUCOSE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHO	84	71
466	9	10467	11006	gi|147403	mannose permease subunit II-P-Man [Escherichia coli]	84	61
497	2	469	1680	gi|1220529	methyl transferase [Streptococcus pneumoniae]	84	72
545	2	309	2171	gi|532548	ORF15 [Enterococcus faecalis]	84	68
550	5	2744	2265	gi|455528	ORF2 [Streptococcus thermophilus bacteriophage]	84	54
637	5	2679	3545	gnl|PID|e236571	cell wall anchoring signal [Enterococcus faecalis]	84	72
653	3	1023	736	gi|1408584	LtrC [Lactococcus lactis lactis]	84	72
674	1	763	254	gi|467452	unknown [Bacillus subtilis]	84	66
788	1	165	500	gi|1196907	daunorubicin resistance protein [Streptomyces peucetius]	84	66

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
796	1	1	366	gi|496504	orf beta [Streptococcus pyogenes]	84	67
812	1	2	415	gi|511075	ORF2 [Streptococcus agalactiae]	84	73
935	2	1317	949	gnl|PID|e247026	orf6 [Lactobacillus sake]	84	73
954	1	3	470	gi|40019	ORF 821 (aa 1-821) [Bacillus subtilis]	84	67
17	3	2922	3311	gi|532555	ORF22 [Enterococcus faecalis]	83	69
17	12	8919	10130	gi|532553	ORF20 [Enterococcus faecalis]	83	64
17	30	30339	29137	gi|467416	unknown [Bacillus subtilis]	83	69
22	4	3208	3453	gi|467469	unknown [Bacillus subtilis]	83	64
28	3	6158	3471	pir|A26738|SYBSVS	valine--tRNA ligase (EC 6.1.1.9) - Bacillus stearothermophilus	83	70
75	2	359	1405	gi|310628	phosphoenolpyruvate:sugar phosphotransferase system enzyme I Streptococcus mutans]	83	72
78	4	6971	5841	gi|155571	alcohol dehydrogenase I (adhA) (EC 1.1.1.1) [Zymomonas mobilis] pir|A35260|A35260 alcohol dehydrogenase (EC 1.1.1.1) I - Zymomonas obilis	83	72
95	9	6859	7521	gi|487280	Na+ -ATPase subunit D [Enterococcus hirae]	83	66
98	3	2785	4008	gi|984803	ATPase [Bacillus subtilis]	83	71
107	3	1467	988	sp|P37214|ERA_STRMU	GTP-BINDING PROTEIN ERA HOMOLOG.	83	73
122	4	2781	3047	gi|467436	unknown [Bacillus subtilis]	83	60
128	3	1572	2633	gi|559471	pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum] pir|S49497|S49497 pyruvate,orthophosphate dikinase (EC 2.7.9.1) - ommon ice plant	83	64
128	34	28154	26844	gi|142941	ftsZ [Bacillus subtilis]	83	69
141	2	555	809	pir|S03556|R3BS18	ribosomal protein S18 - Bacillus stearothermophilus	83	71
173	8	6237	7241	gi|451216	Mannosephosphate Isomerase [Streptococcus mutans]	83	70

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
190	6	3124	2738	gi|532555	ORF22 [Enterococcus faecalis]	83	69
273	1	29	436	gnl|PID|e269878	ribosomal protein S15 [Bacillus subtilis]	83	71
334	1	3	920	gnl|PID|e248484	X-1 [Homo sapiens]	83	71
350	4	2723	2941	gi|511015	dihydroorotate dehydrogenase A [Lactococcus lactis] sp|P54321|PYDA_LACLC DIHYDROOROTATE DEHYDROGENASE A (EC 1.3.3.1) DIHYDROOROTATE OXIDASE A) (DHODEHASE A).	83	66
367	2	1218	529	gi|142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]	83	70
399	23	21538	22989	gi|40025	homologous to E.coli 50K [Bacillus subtilis]	83	67
399	25	25046	25879	gi|43939	D-glucitol-6-P-Dehydrogenase [Klebsiella pneumoniae] ir|S50186|S50186 sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.140) - Klebsiella pneumoniae	83	61
401	7	5097	5864	gi|755153	ATP-binding protein [Bacillus subtilis]	83	64
438	2	217	681	gi|530798	LysB [Bacteriophage phi-LC3]	83	67
497	4	2191	3402	gi|532553	ORF20 [Enterococcus faecalis]	83	63
539	2	2182	782	gi|467475	unknown [Bacillus subtilis]	83	67
563	1	2	1084	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] gnl|PID|e255102 deoxyribodipyrimidine photolyase [Bacillus ubtilis]	83	68
565	4	1018	1206	gi|1123066	weak similarity to bovine cAMP-dependant protein kinase II-B-binding protein (PIR:A39782) [Caenorhabditis elegans]	83	58
577	1	1	561	gi|1303854	YggG [Bacillus subtilis]	83	63
635	3	1210	1527	gi|1402526	ORF5 [Enterococcus faecalis]	83	65
644	1	2	442	gi|153801	enzyme scr-II [Streptococcus mutans]	83	69
655	3	848	1246	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	83	66

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
675	1	1	621	gi|467470	lysyl-tRNA thynthetase [Bacillus subtilis]	83	71
763	2	374	640	gi|145851	envM [Escherichia coli]	83	61
774	1	658	2	gi|1256145	YbbP [Bacillus subtilis]	83	60
3	1	58	327	gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolyticus]	82	70
5	10	6389	7708	sp|P30053|SYH_STREQ	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).	82	71
27	4	1906	1145	gi|1303960	YqjI [Bacillus subtilis]	82	71
32	2	1333	965	gi|1303839	YqfR [Bacillus subtilis]	82	60
34	1	1643	324	gnl|PID|e218042	pyruvate kinase [Lactobacillus delbrueckii]	82	68
55	9	4182	5054	gi|1685110	tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus thermophilus]	82	70
62	7	4644	4210	gi|143723	putative [Bacillus subtilis]	82	66
88	2	995	1624	gi|535349	CodW [Bacillus subtilis]	82	66
94	7	4790	3432	gi|1146247	asparaginyl-tRNA synthetase [Bacillus subtilis]	82	67
110	23	21590	20742	gi|467403	seryl-tRNA synthetase [Bacillus subtilis]	82	69
114	7	8623	9228	gi|703442	thymidine kinase [Streptococcus gordonii]	82	68
123	6	4499	4996	gi|467356	unknown [Bacillus subtilis]	82	68
130	3	1413	2381	gi|308851	ATP binding protein [Lactococcus lactis]	82	64
144	3	3292	2339	gnl|PID|e183449	putative ATP-binding protein of ABC-type [Bacillus subtilis]	82	62
144	7	5331	5110	gi|335495	A23R; putative [Vaccinia virus]	82	47
159	4	2533	5010	gi|143148	transfer RNA-Leu synthetase [Bacillus subtilis]	82	71
159	6	5845	5387	gi|467354	unknown [Bacillus subtilis]	82	55
171	8	8510	9349	gi|1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	82	61
222	5	2158	3402	gi|143444	RNase PH [Bacillus subtilis]	82	66

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
254	6	1621	1112	gi|49316	ORF2 gene product [Bacillus subtilis]	82	61
279	12	9839	8442	gi|1237019	Srb [Bacillus subtilis]	82	67
288	1	22	546	gi|149393	lacA [Lactococcus lactis]	82	73
345	8	5608	8118	gi|442360	ClpC adenosine triphosphatase [Bacillus subtilis]	82	63
367	3	1472	1110	gi|142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]	82	75
367	9	4961	3660	gi|44073	SecY protein [Lactococcus lactis]	82	65
367	28	12719	12411	pir|A02815|R5BS23	ribosomal protein L23 - Bacillus stearothermophilus	82	66
367	29	13330	12701	gi|1165304	L4 [Bacillus subtilis]	82	67
379	5	4396	3107	gi|887820	UUG start; possible frameshift at end? [Escherichia coli]	82	71
393	2	1145	711	gi|1303993	YqkL [Bacillus subtilis]	82	67
416	1	3	650	gi|475113	sucrase [Pediococcus pentosaceus]	82	69
477	1	1	1209	gi|309663	signaling protein [Plasmid pCF10]	82	62
497	7	3760	4275	gi|532551	ORF18 [Enterococcus faecalis]	82	67
535	3	4275	1666	gi|1747434	KdpD [Clostridium acetobutylicum]	82	62
587	1	488	108	gi|1303840	YqfS [Bacillus subtilis]	82	71
623	2	122	1348	gi|460259	enolase [Bacillus subtilis]	82	67
656	1	1	1908	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	82	69
687	1	227	1252	gi|40218	PRPP synthetase (AA 1-317) [Bacillus subtilis]	82	64
728	1	3	527	gi|1146183	putative [Bacillus subtilis]	82	65
741	1	3	704	gi|153804	sucrose-6-phosphate hydrolase [Streptococcus mutans]	82	66
846	1	458	3	gnl|PID|e221400	tex gene product [Bordetella pertussis]	82	76
865	1	18	308	gi|416006	orf CJO1.2 [Campylobacter jejuni]	82	57
876	1	207	689	gi|1064795	function unknown [Bacillus subtilis]	82	62
925	1	436	128	gi|1773195	hypothetical [Escherichia coli]	82	74

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
983	2	280	474	gi|40026	homologous to E.coli gidA [Bacillus subtilis]	82	78
12	3	4778	5788	gi|1100074	tryptophanyl-tRNA synthetase [Clostridium longisporum]	81	68
31	4	2984	4456	gi|849026	hypothetical 54.6-kDa protein [Bacillus subtilis]	81	68
34	6	6707	6910	gi|606067	ORF_f444 [Escherichia coli]	81	54
37	1	1	144	gi|1303854	YqgG [Bacillus subtilis]	81	59
37	3	2671	1958	gi|40056	phoP gene product [Bacillus subtilis]	81	61
57	3	1733	3220	gi|1657506	hypothetical protein [Escherichia coli]	81	66
60	5	5564	4440	gi|143370	phosphoribosylpyrophosphate amidotransferase (PUR-F; EC 2.4.2.14) Bacillus subtilis]	81	63
73	3	2706	1450	gi|853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus ubtilis]	81	61
88	4	1977	2732	gnl|PID|e137596	heat shock induced protein HtpO [Lactobacillus leichmannii]	81	67
88	5	2723	3040	gi|535350	CodX [Bacillus subtilis]	81	65
101	4	3091	2435	gi|1109687	ProZ [Bacillus subtilis]	81	60
101	7	5884	4661	gi|1109684	ProV [Bacillus subtilis]	81	64
101	9	7501	7965	gi|1001768	queuosine biosynthesis protein QueA [Synechocystis sp.]	81	47
116	5	2766	3395	gi|1146234	dihydrodipicolinate reductase [Bacillus subtilis]	81	66
121	5	4811	5074	gi|153765	DNA polymerase I [Streptococcus pneumoniae]	81	64
121	7	5203	7488	gi|153765	DNA polymerase I [Streptococcus pneumoniae]	81	70
127	5	5103	3826	gi|290561	o188 [Escherichia coli]	81	48
147	1	299	1279	gi|467462	cysteine synthetase A [Bacillus subtilis]	81	65
147	2	1370	1861	gnl|PID|e281583	hypothetical 16.4 kd protein [Bacillus	81	63

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					subtilis]		
154	1	168	638	gi|149533	conjugated bile acid hydrolase [Lactobacillus plantarum]	81	66
154	2	1074	1277	gnl|PID|e242898	aBIR [Lactococcus lactis]	81	59
158	14	13790	12324	gi|558559	pyrimidine nucleoside phosphorylase [Bacillus subtilis]	81	71
164	5	2469	3035	gi|727436	putative 20-kDa protein [Lactococcus lactis]	81	61
223	8	5293	6153	gnl|PID|e254976	hypothetical protein [Bacillus subtilis]	81	66
238	1	185	937	gi|622991	mannitol transport protein [Bacillus stearothermophilus] sp|P50852|PTMB_BACST PTS SYSTEM, MANNITOL-SPECIFIC IIBC COMPONENT EIIBC-MTL) (MANNITOL- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE NZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-MTL).	81	68
276	7	3109	2819	pir|A41207|A41207	collagen 13, nonfibrillar - freshwater sponge (Ephydatia muelleri) (fragment)	81	77
307	2	1983	3617	gi|153742	dextran glucosidase [Streptococcus mutans]	81	69
322	2	122	286	gi|296147	Asd protein [Bacillus subtilis]	81	63
326	6	5352	4513	gi|40041	pyruvate dehydrogenase (lipoamide) [Bacillus stearothermophilus] ir|S10798|DEBSPF pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) pha chain - Bacillus stearothermophilus	81	69
329	3	1774	1448	gi|1117994	surface antigen A variant precursor [Streptococcus pneumoniae]	81	72
346	3	1056	1199	gi|536970	ORF_f543 [Escherichia coli]	81	43
362	4	1131	2213	gi|1001826	cadmium-transporting ATPase [Synechocystis sp.]	81	64
391	3	1345	575	gi|1184967	ScrR [Streptococcus mutans]	81	66
441	3	1873	3447	gi|1742675	Phosphotransferase system enzyme II (EC 2.7.1.69) MalX [Escherichia coli]	81	64

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
556	2	1062	493	gi|1553037	RecN [Bacillus subtilis]	81	66
710	2	361	816	gi|1303840	YqfS [Bacillus subtilis]	81	68
804	1	403	2	gi|149533	conjugated bile acid hydrolase [Lactobacillus plantarum]	81	68
5	7	3311	4255	gi|407881	stringent response-like protein [Streptococcus equisimilis] pir|S39975|S39975 stringent response-like protein - Streptococcus quisimilis	80	62
17	10	8283	8438	gi|1326394	B0218.7 gene product [Caenorhabditis elegans]	80	53
17	15	12258	12776	gi|532551	ORF18 [Enterococcus faecalis]	80	63
22	1	3	2180	gi|44027	Tma protein [Lactococcus lactis]	80	70
37	6	3707	5140	pir|B47154|B47154	signal recognition particle 54K chain homolog Ffh - Bacillus subtilis	80	64
42	1	2	259	gi|1066157	chaperonin-10 [Thermus aquaticus thermophilus]	80	66
49	16	11106	11309	gi|1136430	similar to hypothetical protein YM9959.11C of S.cerevisiae. [Homo sapiens]	80	53
60	4	4465	3407	gi|143371	phosphoribosyl aminoimidazole synthetase (PUR-M) [Bacillus subtilis] pir|H29326|AJBSCL phosphoribosylformylglycinamidine cyclo-ligase EC 6.3.3.1) - Bacillus subtilis	80	62
60	9	9023	8745	pir|E29326|E29326	hypothetical protein (pur operon) - Bacillus subtilis	80	50
66	1	1	783	gi|520753	DNA topoisomerase I [Bacillus subtilis]	80	66
80	3	2519	1821	gnl|PID|e236074	beta-phosphoglucomutase [Lactococcus lactis]	80	62
83	9	6268	5378	gi|1070079	R08B4.1 [Caenorhabditis elegans]	80	72
89	18	19093	18845	gi|39451	type III restriction endonuclease [Bacillus cereus] ir|S15518|JC1116 type III site-specific deoxyribonuclease (EC	80	72

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					1.21.5) - Bacillus cereus (fragment)		
97	1	366	4	gi|148506	dnaJ [Erysipelothrix rhusiopathiae]	80	70
107	2	1094	591	sp|P37214|ERA_STRMU	GTP-BINDING PROTEIN ERA HOMOLOG.	80	64
114	3	1474	5076	gi|43863	pyruvate-flavodoxin oxidoreductase [Klebsiella pneumoniae] ir|S01997|QQKBFP pyruvate (flavodoxin) dehydrogenase (EC 1.2.99.-) Klebsiella pneumoniae	80	62
117	3	1456	2367	gi|40031	spoOJ93 gene product [Bacillus subtilis]	80	56
126	3	1857	709	gi|551854	ORF2 [Erwinia herbicola]	80	68
128	28	23265	22447	gi|437916	isoleucyl-tRNA synthetase [Staphylococcus aureus]	80	63
133	10	9128	9856	gi|520844	orf4 [Bacillus subtilis]	80	63
158	4	3926	2703	gi|944943	phosphopentomutase [Bacillus subtilis]	80	64
172	5	3732	3920	sp|P20182|YT14_STRFR	HYPOTHETICAL 29.1 KD PROTEIN IN TRANSPOSON TN4556.	80	63
180	16	15548	16393	gi|1773200	hypothetical protein [Escherichia coli]	80	66
181	10	8597	7407	gi|143806	AroF [Bacillus subtilis]	80	64
194	4	1580	1957	gi|47394	5-oxoprolyl-peptidase [Streptococcus pyogenes]	80	66
213	5	3515	4078	gnl|PID|e199384	pyrR gene product [Lactobacillus plantarum]	80	65
217	11	7724	8395	gi|1561567	Unknown [Bacillus subtilis]	80	65
218	6	4843	5331	gi|1574120	branched-chain-amino-acid transaminase [Haemophilus influenzae]	80	64
225	8	6092	5829	gi|530459	similar to phosphotransferase EII [Mycoplasma capricolum]	80	52
229	2	1170	178	gi|1502419	PlsX [Bacillus subtilis]	80	59
243	3	2545	2150	gi|1732315	transport system permease homolog [Listeria monocytogenes]	80	64
275	2	694	939	gi|1256629	cold-shock protein [Bacillus subtilis]	80	65

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
307	3	3607	3888	gi|1321625	exo-alpha-1, 4-glucosidase [Bacillus stearothermophilus]	80	73
322	3	284	1090	gi|142828	aspartate semialdehyde dehydrogenase [Bacillus subtilis] sp|Q04797|DHAS_BACSU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC .2.1.11) (ASA DEHYDROGENASE).	80	62
349	1	2	616	gi|495089	recombinase [Staphylococcus aureus]	80	65
367	7	3511	2924	gi|44074	adenylate kinase [Lactococcus lactis]	80	64
386	7	4305	5306	gi|149396	lacD [Lactococcus lactis]	80	64
394	3	2642	3757	pir|B39096|B39096	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis	80	64
399	17	12070	13488	gi|1591862	oxaloacetate decarboxylase, alpha subunit [Methanococcus jannaschii]	80	61
399	24	22979	24907	gi|40026	homologous to E.coli gidA [Bacillus subtilis]	80	67
435	3	2217	2032	gi|559863	clyA [Plasmid pAD1]	80	78
466	1	3	1208	gi|467330	replicative DNA helicase [Bacillus subtilis]	80	61
475	4	3402	2947	gi|532547	ORF14 [Enterococcus faecalis]	80	68
491	4	3844	4392	gi|473892	large-conductance mechanosensitive channel [Escherichia coli] gi|473420 yhdC [Escherichia coli]	80	56
605	2	1252	338	gi|580875	ipa-57d gene product [Bacillus subtilis]	80	69
615	1	760	14	gi|467469	unknown [Bacillus subtilis]	80	66
668	1	117	587	pir|S16974|R5BS7F	ribosomal protein L9 - Bacillus stearothermophilus	80	71
684	2	694	464	gi|786314	Highly similar to Glycogen debranching enzyme 4-alpha-glucanotransferase, Swiss Prot. accession number P35573) Saccharomyces cerevisiae]	80	33
767	1	1	480	gi|41828	istB gene product [Escherichia coli]	80	52
818	1	1	357	gi|1743856	intrageneric coaggregation-relevant	80	66

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					adhesin [Streptococcus gordonii]		
833	1	325	95	gi|1561567	Unknown [Bacillus subtilis]	80	68
934	1	394	56	gi|1001706	ABC transporter subunit [Synechocystis sp.]	80	63
948	1	465	4	gi|1773196	similar to B. stearothermophilus N-carbamyl-L-amino acid amidohydrolase [Escherichia coli]	80	59
949	1	61	411	gi|1330380	Similar to cystathionine gamma-lyase [Caenorhabditis elegans]	80	61
20	2	468	1262	gi|1256698	chitinase [Serratia marcescens]	79	67
22	3	2420	3238	gi|467460	unknown [Bacillus subtilis]	79	59
24	1	39	1109	gi|1303821	YqfE [Bacillus subtilis]	79	61
26	1	214	873	gi|403984	deoxyguanosine kinase/deoxyadenosine kinase(I) subunit Lactobacillus acidophilus]	79	68
47	8	10268	8106	gi|153657	mismatch repair protein [Streptococcus pneumoniae] pir|A33589|A33589 mismatch repair protein hexB - Streptococcus neumoniae	79	63
48	9	9905	9198	gi|290566	f213 [Escherichia coli]	79	53
58	4	4677	3694	gi|1653179	hydrogenase subunit [Synechocystis sp.]	79	52
63	6	3605	5443	gi|1064813	homologous to sp:PHOR_BACSU [Bacillus subtilis]	79	55
88	8	5493	4771	gnl|PID|e208252	unidentified [Streptococcus pneumoniae]	79	57
146	8	6649	5609	gi|153676	tagatose 1,6-aldolase [Streptococcus mutans]	79	63
149	4	2554	1976	gi|1216490	DNA/pantothenate metabolism flavoprotein [Streptococcus mutans]	79	64
158	2	1859	1143	gi|1276873	DeoD [Streptococcus thermophilus]	79	67
179	19	19022	18417	gi|467372	3'-exo-deoxyribonuclease [Bacillus subtilis]	79	61
222	2	982	230	gi|142988	membrane transport protein [Bacillus	79	59

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					stearothermophilus] pir|A42478|A42478 glutamine transport protein glnQ - Bacillus tearothermophilus		
228	6	4060	3401	gi|413950	ipa-26d gene product [Bacillus subtilis]	79	55
229	3	3270	1219	gnl|PID|e186699	MmsA [Streptococcus pneumoniae]	79	62
238	7	5750	5100	gi|596046	L8003.16 gene product [Saccharomyces cerevisiae]	79	55
269	10	6664	5489	gi|1303788	YqeH [Bacillus subtilis]	79	63
274	1	1	1143	gi|153062	helicase [Staphylococcus aureus]	79	65
290	9	7364	8779	gi|466882	pps1; B1496_C2_189 [Mycobacterium leprae]	79	64
292	22	18122	17595	gi|1303951	YqiZ [Bacillus subtilis]	79	61
316	3	864	2003	gi|1146207	putative [Bacillus subtilis]	79	58
326	2	1772	360	gi|40044	dihydrolipoamide dehydrogenase [Bacillus stearothermophilus] ir|S13839|S13839 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - cillus stearothermophilus	79	65
363	5	5738	7180	gi|1657519	hypothetical protein [Escherichia coli]	79	63
367	11	5668	5447	gi|216337	ORF for L30 ribosomal protein [Bacillus subtilis]	79	63
375	5	4346	3393	gi|1644203	unknown [Bacillus subtilis]	79	62
406	2	666	1481	gi|49316	ORF2 gene product [Bacillus subtilis]	79	58
460	7	4973	5860	gi|1276664	acetyl-CoA carboxylase carboxytransferase beta subunit [Porphyra purpurea]	79	62
486	1	380	3	gi|1256618	transport protein [Bacillus subtilis]	79	63
488	3	987	1997	gi|532547	ORF14 [Enterococcus faecalis]	79	69
500	2	1358	681	gi|535662	transposase [Insertion sequence IS1251]	79	75
523	3	1803	820	gi|142981	ORF5; This ORF includes a region (aa23-103) containing a potential ron-sulphur centre homologous to a region of Rhodospirillum rubrum nd Chromatium vinosum; putative [Bacillus stearothermophilus] pir|PQ0299|PQ0299	79	62

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					hypothetical protein 5 (gldA 3' region) -		
552	2	2401	902	gi|887851	ORF_o479 [Escherichia coli]	79	63
587	2	622	434	gi|1303840	YqfS [Bacillus subtilis]	79	66
612	1	1	378	gi|1064791	function umknown [Bacillus subtilis]	79	56
654	1	2	286	pir|A47079|A47079	heat shock protein DnaJ - Lactococcus lactis	79	75
701	2	325	534	gi|143793	tyrosyl-tRNA synthetase [Bacillus caldotenax]	79	63
708	2	369	566	gi|488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	79	66
840	1	140	1078	gi|1573250	aspartate aminotransferase (aspC) [Haemophilus influenzae]	79	65
5	9	5555	6049	gi|407880	ORF1 [Streptococcus equisimilis]	78	58
33	4	3755	4597	gi|1742846	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1) (Nitrogen-regulatory protein). [Escherichia coli]	78	64
60	7	8100	5854	gi|143369	phosphoribosylformyl glycinamidine synthetase II (PUR-Q) [Bacillus ubtilis]	78	62
65	4	3407	2625	gi|1661179	high affinity branched chain amino acid transport protein [Streptococcus mutans]	78	67
76	7	5760	4747	gi|1161061	dioxygenase [Methylobacterium extorquens]	78	62
81	11	7141	6824	gi|1072380	ORF3 [Lactococcus lactis]	78	67
83	5	2559	2843	gi|1256896	L9606.1 gene product [Saccharomyces cerevisiae]	78	52
85	4	4298	3288	gi|142612	branched chain alpha-keto acid dehydrogenase E1-beta [Bacillus ubtilis]	78	61
85	8	6723	6307	gi|1303941	YqiV [Bacillus subtilis]	78	62
88	10	6477	6689	gi|222585	nucleocapsid protein [Sialodacryoadenitis virus]	78	57
93	5	1838	2641	gi|405133	putative [Bacillus subtilis]	78	51
117	1	3	707	gi|40027	homologous to E.coli gidB [Bacillus	78	64

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					subtilis]		
117	11	9624	8338	gi|467403	seryl-tRNA synthetase [Bacillus subtilis]	78	63
132	2	2323	2024	gi|683484	fusion protein [Mumps virus]	78	63
133	3	2241	3413	gi|405622	unknown [Bacillus subtilis]	78	63
150	2	568	1425	gnl|PID|e185373	ceuD gene product [Campylobacter coli]	78	52
155	2	604	1182	gi|285628	transcription antitermination factor NusG [Bacillus subtilis] pir|S39859|S39859 transcription antitermination factor NusG - acillus subtilis	78	61
156	2	308	2629	gi|1573874	ATP-dependent protease binding subunit (clpB) [Haemophilus influenzae]	78	59
158	3	2719	1868	gi|1638804	purine nucleoside phosphorylase [Bacillus stearothermophilus]	78	64
160	5	2058	3050	gi|1161061	dioxygenase [Methylobacterium extorquens]	78	60
161	3	1466	3295	gnl|PID|e280490	unknown [Streptococcus pneumoniae]	78	62
169	1	2	2206	gi|1072361	pyruvate-formate-lyase [Clostridium pasteurianum]	78	61
171	2	2833	3897	sp|P28367|RF2_BACSU	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) (FRAGMENT).	78	64
180	15	14851	15567	gi|1773199	hypothetical protein [Escherichia coli]	78	67
185	1	1142	3	pir|C33496|C33496	hisC homolog - Bacillus subtilis	78	59
188	3	1863	4178	gnl|PID|e256969	nifJ gene product [Enterobacter agglomerans]	78	62
216	7	5136	5600	gnl|PID|e276830	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	78	60
216	8	5531	6508	gnl|PID|e276830	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	78	63
238	26	24515	25387	gi|396681	rhamnulose-1-phosphate aldolase [Escherichia coli]	78	56
256	6	4189	6237	gi|467427	methionyl-tRNA synthetase [Bacillus	78	67

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					subtilis]		
292	4	2063	2353	gi|1742823	Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein). [Escherichia coli]	78	62
305	1	268	1872	gi|143582	spoIIIEA protein [Bacillus subtilis]	78	58
337	2	2332	1448	gi|308861	GTG start codon [Lactococcus lactis]	78	63
338	2	606	1466	gi|1773142	similar to the 20.2kd protein in TETB-EXOA region of B. subtilis [Escherichia coli]	78	66
362	1	109	429	gi|150719	cadmium resistance protein [Plasmid pI258]	78	51
379	3	2878	1922	gi|887824	ORF_o310 [Escherichia coli]	78	60
446	2	962	1636	gi|537235	Kenn Rudd identifies as gpmB [Escherichia coli]	78	43
495	5	3038	3502	gi|634107	kdpB [Escherichia coli]	78	58
502	3	3077	1470	gi|1652592	peptide-chain-release factor 3 [Synechocystis sp.]	78	58
523	1	2	616	gi|289288	lexA [Bacillus subtilis]	78	59
571	1	99	365	gnl|PID|e249644	YneF [Bacillus subtilis]	78	65
573	3	1258	1971	gi|1731683	component II of heptaprenyl diphosphate synthase [Bacillus stearothermophilus]	78	50
575	2	434	168	gi|58831	The experimental evidence that this sequence codes for a complete gag otein is that transfection of the viral genome results in oduction of infectious virus [Cas-Br-E murine leukemia virus] p|P27460|GAG_MLVCB GAG POLYPROTEIN (CONTAINS: CORE PROTEIN P15; N	78	47
607	1	148	708	gi|530410	Ala-tRNA synthetase [Mycoplasma capricolum]	78	63
655	2	300	899	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	78	60
704	1	181	2	gi|467430	unknown [Bacillus subtilis]	78	63
708	1	1	378	gi|443985	alcohol dehydrogenase [Entamoeba	78	61

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					histolytica]		
732	1	661	2	gi|1064791	function umknown [Bacillus subtilis]	78	55
785	1	2	679	gi|556014	UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis]	78	59
786	1	2	172	gi|536992	SugES [Escherichia coli]	78	60
820	2	1602	1144	gi|153749	UDPglucose 4-epimerase [Streptococcus thermophilus] pir|A44509|A44509 UDPglucose 4-epimerase (EC 5.1.3.2) - treptococcus thermophilus	78	60
887	1	337	2	gi|495046	tripeptidase [Lactococcus lactis]	78	70
970	2	395	234	gi|1652190	Fat protein [Synechocystis sp.]	78	51
4	7	6069	5656	gi|1573482	high affinity ribose transport protein (rbsD) [Haemophilus influenzae]	77	51
45	16	12065	14047	gi|666069	orf2 gene product [Lactobacillus leichmannii]	77	51
49	13	8199	9992	gnl|PID|e228615	homologous to yqcC of the skin element [Bacillus subtilis]	77	59
60	2	2895	1300	gi|143373	phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) Bacillus subtilis]	77	63
70	6	5118	3874	gi|912464	No definition line found [Escherichia coli]	77	53
70	7	5172	5756	gi|288413	glutamate dehydrogenase (NADP+) [Corynebacterium glutamicum] pir|S32227|S32227 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - orynebacterium glutamicum	77	65
74	10	7303	5864	gi|289284	cysteinyl-tRNA synthetase [Bacillus subtilis]	77	62
74	12	9559	8078	gi|289282	glutamyl-tRNA synthetase [Bacillus subtilis]	77	57

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
88	6	3013	3843	gi|535351	CodY [Bacillus subtilis]	77	57
89	6	5749	2510	gi|1695686	pyruvate carboxylase [Bacillus stearothermophilus]	77	62
91	1	396	728	gi|1184044	L-glutamine:D-fructose-6-P amidotransferase precursor [Thermus aquaticus thermophilus]	77	66
98	4	3992	5710	gi|984804	transmembrane protein [Bacillus subtilis]	77	56
124	1	2	940	gnl|PID|e199002	prolidase PepQ [Lactobacillus delbrueckii]	77	60
158	5	4845	4171	gi|435297	unknown [Lactococcus lactis]	77	48
162	6	7426	5882	gi|142992	glycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir|B45868|B45868 glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp|P18157|GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL - PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK).	77	60
164	1	179	1102	gi|882532	ORF_o294 [Escherichia coli]	77	57
164	22	24158	23646	gi|1573564	hypothetical [Haemophilus influenzae]	77	36
171	6	6656	7639	gi|1303855	YqgH [Bacillus subtilis]	77	59
171	9	9198	9683	gi|1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	77	57
202	4	2967	3422	gi|147782	ruvA protein (gtg start) [Escherichia coli]	77	50
202	6	3662	4693	gi|147783	ruvB protein [Escherichia coli]	77	58
213	1	3	1046	gi|1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	77	63
217	10	6870	7742	gi|414014	ipa-90d gene product [Bacillus subtilis]	77	50
223	5	4171	4902	gnl|PID|e254974	autolysin response regulator [Bacillus subtilis]	77	55
223	7	5024	5473	gnl|PID|e254975	hypothetical protein [Bacillus subtilis]	77	58
228	10	7747	6035	gi|467409	DNA polymerase III subunit [Bacillus subtilis]	77	61
229	15	16711	14261	gnl|PID|e290286	priA [Bacillus subtilis]	77	62

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

C ntig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
232	3	1742	1437	gi|142708	comG3 gene product [Bacillus subtilis]	77	50
238	25	23174	24511	pir|B48649|B48649	L-rhamnose isomerase (EC 5.3.1.14) - Escherichia coli	77	59
238	32	29472	28708	gi|451072	di-tripeptide transporter [Lactococcus lactis]	77	56
244	4	3591	2809	gi|1773173	similar to M. jannaschii MJ0938 [Escherichia coli]	77	60
269	5	3890	3522	gi|1303793	YqeL [Bacillus subtilis]	77	55
276	6	2840	2328	pir|PC1127|PC1127	hypothetical 110 protein (lytA 5' region) - Lactococcus lactis phage US3 (fragment)	77	50
291	1	119	916	gi|556014	UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis]	77	63
304	2	941	2020	gnl|PID|e285001	CTORF239 [Staphylococcus aureus]	77	62
305	4	3618	4394	gi|709993	hypothetical protein [Bacillus subtilis]	77	54
327	8	5697	6005	gi|153570	H+ ATPase [Enterococcus faecalis]	77	61
341	4	1206	1937	gi|1303951	YqiZ [Bacillus subtilis]	77	62
360	1	429	4	gi|897754	nonstructural protein NSP3 [Human rotavirus]	77	38
362	3	541	1239	gi|1001826	cadmium-transporting ATPase [Synechocystis sp.]	77	60
363	9	13917	12652	gi|1574390	C4-dicarboxylate transport protein [Haemophilus influenzae]	77	55
367	14	7218	6679	pir|A02766|R5BS0F	ribosomal protein L6 - Bacillus stearothermophilus	77	63
386	8	5456	5776	gnl|PID|e281578	hypothetical 12.2 kd protein [Bacillus subtilis]	77	61
394	4	3706	4167	pir|B39096|B39096	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis	77	55
402	1	710	3	gi|533105	unknown [Bacillus subtilis]	77	59
408	2	1357	584	gi|666983	putative ATP binding subunit [Bacillus subtilis]	77	58

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
460	6	3562	4938	gi|1055246	biotin carboxylase [Bacillus subtilis]	77	60
466	7	8657	9253	gi|147402	mannose permease subunit III-Man [Escherichia coli]	77	61
475	5	3794	3234	gi|532547	ORF14 [Enterococcus faecalis]	77	68
498	1	1	603	gi|410137	ORFX13 [Bacillus subtilis]	77	58
515	1	107	574	gi|1303815	YqeY [Bacillus subtilis]	77	60
518	6	2980	4518	gi|1402515	membrane-spanning transporter protein [Clostridium perfringens]	77	56
523	5	2527	2333	gi|149601	thymidylate synthase (EC 2.1.1.45) [Lactobacillus casei]	77	66
526	2	1782	436	gi|1750124	xylose isomerase [Bacillus subtilis]	77	62
552	7	6809	6135	gi|534045	antiterminator [Bacillus subtilis]	77	51
607	3	778	936	gi|1015321	alanyl-tRNA synthetase [Homo sapiens]	77	51
624	3	2289	2555	gnl|PID|e187971	orf121 gene product [Lactococcus lactis]	77	57
781	1	15	485	gi|580883	ipa-88d gene product [Bacillus subtilis]	77	65
850	2	895	572	gi|142520	thioredoxin [Bacillus subtilis]	77	59
853	1	186	4	gi|39962	ribosomal protein L35 (AA 1-66) [Bacillus stearothermophilus] ir|S05347|R5BS35 ribosomal protein L35 - Bacillus earothermophilus	77	66
944	1	2	172	gi|425467	transposase [Lactobacillus helveticus]	77	50
10	1	1	258	gnl|PID|e234078	hom [Lactococcus lactis]	76	63
12	4	7650	5842	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	76	57
17	29	29022	28153	gi|1500003	mutator mutT protein [Methanococcus jannaschii]	76	47
23	15	8897	10285	gi|153960	ethanolamine ammonia-lyase (eutB) [Salmonella typhimurium] pir|A36570|A36570 ethanolamine ammonia-lyase (EC 4.3.1.7) 55K chain Salmonella typhimurium	76	64
29	2	1024	500	gi|40011	ORF17 (AA 1-161) [Bacillus subtilis]	76	61
33	1	14	1552	gi|148304	beta-1,4-N-acetylmuramoylhydrolase	76	60

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Enterococcus hirae] pir|A42296|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790)		
34	7	7432	6965	gi|44067	ORF1 C-terminal [Lactococcus lactis]	76	59
45	8	3708	4166	gi|1303698	BltD [Bacillus subtilis]	76	56
47	9	12849	10270	gi|1002520	MutS [Bacillus subtilis]	76	59
55	8	3614	4105	gi|1303915	YghZ [Bacillus subtilis]	76	53
55	11	6385	6642	gi|216583	ORF1 [Escherichia coli]	76	45
57	14	17283	16597	gi|1183887	integral membrane protein [Bacillus subtilis]	76	56
59	6	3112	2426	gi|392872	repressor protein [Pasteurella multocida]	76	47
64	1	1242	46	gi|483941	blt gene product [Bacillus subtilis]	76	55
67	3	1370	2146	gnl|PID|e199390	orotate phosphoribosyltransferase [Lactobacillus plantarum]	76	57
69	2	837	334	gi|1377831	unknown [Bacillus subtilis]	76	57
70	1	164	1588	gi|895751	putative 6-phospho-beta-glucosidase [Bacillus subtilis] pir|S57762|S57762 probable 6-phospho-beta-glucosidase - Bacillus ubtilis	76	60
74	11	7826	7269	pir|E53402|E53402	serine O-acetyltransferase (EC 2.3.1.30) - Bacillus stearothermophilus	76	54
74	13	10073	9588	gi|289281	unknown [Bacillus subtilis]	76	60
85	11	7809	7102	gi|457634	butyrate kinase [Clostridium acetobutylicum]	76	61
94	8	6036	4801	gi|142538	aspartate aminotransferase [Bacillus sp.]	76	57
94	14	17174	12801	gi|40060	DNA polymerase III (AA 1-1437) [Bacillus subtilis] p|P13267|DP3A_BACSU DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7).	76	62
94	15	19140	17407	gi|1573733	prolyl-tRNA synthetase (proS) [Haemophilus influenzae]	76	54
95	1	1	1290	gi|472918	v-type Na-ATPase [Enterococcus hirae]	76	59

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
95	4	2367	3194	gi|487276	Na+ -ATPase subunit C [Enterococcus hirae]	76	48
99	1	1	171	gi|1353874	unknown [Rhodobacter capsulatus]	76	52
100	5	5414	5064	gi|1591962	M. jannaschii predicted coding region MJ1322 [Methanococcus jannaschii]	76	46
100	27	23165	21198	gi|216151	DNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi|579197 SP02 DNA polymerase (aa 1-648) [Bacteriophage SPO2] pir|A21498|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage PO2	76	62
106	1	1511	264	gi|1750108	YnbA [Bacillus subtilis]	76	61
116	4	2480	2854	gi|755602	unknown [Bacillus subtilis]	76	60
116	6	3299	3625	gi|1146234	dihydrodipicolinate reductase [Bacillus subtilis]	76	56
122	5	3029	3619	gi|467436	unknown [Bacillus subtilis]	76	52
123	10	9109	10389	gi|1773196	similar to B. stearothermophilus N-carbamyl-L-amino acid amidohydrolase [Escherichia coli]	76	61
124	5	4087	3182	gi|974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus ubtilis]	76	58
130	5	3341	4294	gi|308853	transmembrane protein [Lactococcus lactis]	76	55
132	3	2265	5117	gi|1673889	(AE000022) Mycoplasma pneumoniae, excinuclease ABC subunit A; similar to Swiss-Prot Accession Number P07671, from E. coli [Mycoplasma pneumoniae]	76	59
138	34	25849	25409	gi|143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	76	56
139	1	3	350	gnl|PID|e191395	mobilisation protein [Lactococcus lactis]	76	65
141	1	2	544	gi|662792	single-stranded DNA binding protein [unidentified eubacterium]	76	64
155	9	7612	7058	gnl|PID|e247026	orf6 [Lactobacillus sake]	76	57
164	4	1889	2416	gi|727436	putative 20-kDa protein [Lactococcus lactis]	76	55

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
181	5	3475	2288	gi|1147744	PSR [Enterococcus hirae]	76	53
181	8	6281	4986	gi|683583	5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus lactis] pir|S52580|S52580 3-phosphoshikimate 1-carboxyvinyltransferase (EC .5.1.19) - Lactococcus lactis	76	62
197	7	7662	8102	gi|1783253	homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis]	76	58
222	16	10780	11298	gi|1591856	hypothetical protein (SP:P15889) [Methanococcus jannaschii]	76	64
229	1	1	138	gi|148316	NaH-antiporter protein [Enterococcus hirae]	76	47
233	6	3946	3341	gi|1591652	hypothetical protein (SP:P31065) [Methanococcus jannaschii]	76	60
238	2	844	1848	gi|622991	mannitol transport protein [Bacillus stearothermophilus] sp|P50852|PTMB_BACST PTS SYSTEM, MANNITOL-SPECIFIC IIBC COMPONENT EIIBC-MTL) (MANNITOL- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE NZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-MTL).	76	64
238	9	7235	7957	gi|1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	76	49
249	2	543	1235	gi|143156	membrane bound protein [Bacillus subtilis]	76	45
262	3	4131	2692	gnl|PID|e281591	catalase [Bacillus subtilis]	76	65
265	1	2	400	gi|141858	replication-associated protein [Plasmid pAD1]	76	52
271	13	8175	10844	gi|397973	Mg2+ transport ATPase [Salmonella typhimurium]	76	57
323	4	4128	4568	gnl|PID|e249023	T19B10.3 [Caenorhabditis elegans]	76	60
329	5	3270	2560	gi|310631	ATP binding protein [Streptococcus gordonii]	76	54
356	1	971	3	gi|971479	orf3 gene product [Lactobacillus	76	52

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					delbrueckii]		
371	1	1564	944	gi|1750125	xylulose kinase [Bacillus subtilis]	76	57
375	6	5137	4238	gi|1644202	unknown [Bacillus subtilis]	76	58
382	2	508	2769	gi|442360	ClpC adenosine triphosphatase [Bacillus subtilis]	76	60
399	11	7811	8845	gi|1572970	acetate:SH-citrate lyase ligase (AMP) [Haemophilus influenzae]	76	54
399	13	9126	10034	gi|1572968	citrate lyase beta chain (acyl lyase subunit) (citE) [Haemophilus influenzae]	76	57
485	1	3	1262	gi|564018	dihydrofolate synthetase [Streptococcus pneumoniae]	76	54
486	2	970	344	gi|1256617	adenine phosphoribosyltransferase [Bacillus subtilis]	76	61
536	1	220	2	gi|437389	transposase [Lactococcus lactis]	76	59
552	3	3969	2491	gi|882609	6-phospho-beta-glucosidase [Escherichia coli]	76	63
634	2	697	918	gi|1022725	unknown [Staphylococcus haemolyticus]	76	52
684	3	1191	688	gi|1256653	DNA-binding protein [Bacillus subtilis]	76	65
752	1	1111	929	gi|407907	ORF2 [Staphylococcus xylosus]	76	46
822	1	548	237	gi|144313	6.0 kd ORF [Plasmid ColE1]	76	73
923	1	2	421	gi|153843	trypsin-resistant surface T6 protein (tee6) precursor [Streptococcus yogenes]	76	57
953	2	534	187	gi|1592339	hypothetical protein (PIR:S52522) [Methanococcus jannaschii]	76	44
965	2	564	343	gi|1098898	CTRP [Plasmodium falciparum]	76	69
7	4	3754	4161	gi|495046	tripeptidase [Lactococcus lactis]	75	61
25	1	2	580	gi|1575577	DNA-binding response regulator [Thermotoga maritima]	75	57
45	7	3090	3350	gi|1673663	(AE000003) Mycoplasma pneumoniae, E07_orf166 Protein [Mycoplasma pneumoniae]	75	35
47	6	7526	6957	gi|1673843	(AE000019) Mycoplasma pneumoniae, pilB	75	58

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					homolog; similar to GenBank Accession Number E64124, from H. influenzae [Mycoplasma pneumoniae]		
51	1	15	1520	sp|P39168|ATMA_ECOLI	MG(2+) TRANSPORT ATPASE, P-TYPE 1 (EC 3.6.1.-).	75	58
54	11	3761	3579	gi|1504026	similar to C.elegans protein (Z37093) [Homo sapiens]	75	56
55	5	1648	2562	gi|1303901	YqhT [Bacillus subtilis]	75	58
56	8	5873	5358	gi|895749	putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis]	75	49
58	2	2707	1916	gi|1658403	formate dehydrogenase alpha subunit [Moorella thermoacetica]	75	58
71	1	110	1429	gi|1304007	LysA [Bacillus subtilis]	75	58
74	5	3436	3074	gi|467433	unknown [Bacillus subtilis]	75	61
74	8	5491	4631	gi|467483	unknown [Bacillus subtilis]	75	60
77	1	3	992	gi|1653966	47 kD protein [Synechocystis sp.]	75	34
81	1	26	862	gi|1064809	homologous to sp:HTRA_ECOLI [Bacillus subtilis]	75	55
89	11	11651	9801	gi|1573881	hypothetical [Haemophilus influenzae]	75	51
96	3	2521	1643	gi|1531619	NodB [Rhizobium sp.]	75	54
98	9	11494	10199	gi|1573043	hypothetical [Haemophilus influenzae]	75	53
110	12	11326	10283	gi|1184121	auxin-induced protein [Vigna radiata]	75	51
117	13	11200	9944	gi|457635	vancomycin histidine protein kinase [Enterococcus faecium] gi|801884 vanS [Transposon Tn1546]	75	51
122	6	3812	5206	gi|467439	temperature sensitive cell division [Bacillus subtilis]	75	59
128	12	8262	7921	gi|466473	cellobiose phosphotransferase enzyme II' [Bacillus tearothermophilus]	75	48
128	38	31848	30733	gi|216300	peptidoglycan synthesis enzyme [Bacillus subtilis] sp|P37585|MURG_BACSU MURG PROTEIN UPD-N-ACETYLGLUCOSAMINE--N-	75	56

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					ACETYLMURAMYL-PENTAPEPTIDE)PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE RANSFERASE).		
129	2	1916	2134	gnl|PID|e267624	Unknown, highly similar to Pseudomonas putida 4-oxalocrotonate tautomerase [Bacillus subtilis]	75	47
130	4	2375	3343	gi|495179	transmembrane protein [Lactococcus lactis]	75	55
133	1	3	1514	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	75	54
158	13	12326	11634	gi|809660	deoxyribose-phosphate aldolase [Bacillus subtilis] pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	75	66
162	13	14285	12543	gi|1653222	cation-transporting ATPase PacL [Synechocystis sp.]	75	60
170	2	1280	921	sp|P07999|DHGB_BACME	GLUCOSE 1-DEHYDROGENASE B (EC 1.1.1.47).	75	62
171	7	7618	8523	gi|1303856	YqgI [Bacillus subtilis]	75	52
179	14	14668	15255	gi|457177	alkyl hydroperoxide reductase [Salmonella typhimurium] sp|P19479|AHPC_SALTY ALKYL HYDROPEROXIDE REDUCTASE C22 PROTEIN (EC .6.4.-). {SUB 2-187}	75	55
181	6	4470	3604	gi|683585	prephenate dehydratase [Lactococcus lactis]	75	49
191	1	183	560	gnl|PID|e261991	putative orf [Bacillus subtilis]	75	57
197	3	2117	3592	gi|1783250	homologous to cytochrome d ubiquinol oxidase subunit I; hypothetical [Bacillus subtilis]	75	60
215	3	2545	2201	gnl|PID|e284996	ORF136 [Staphylococcus aureus]	75	54
216	1	2	256	gi|153570	H+ ATPase [Enterococcus faecalis]	75	53
223	4	2406	4193	gi|862312	lytS gene product [Staphylococcus aureus]	75	56
227	5	3004	3567	gi|144729	butanol dehydrogenase [Clostridium acetobutylicum] sp|Q04944|ADHA_CLOAB NADH-	75	53

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					DEPENDENT BUTANOL DEHYDROGENASE A (EC .1.1.-) (BDH I).		
228	9	6032	5700	gi|467410	unknown [Bacillus subtilis]	75	59
229	16	17081	16848	gi|207398	tropomyosin T class IVd alpha-3 [Rattus norvegicus]	75	42
238	8	6038	7237	gi|141927	czcB gene product [Alcaligenes eutrophus]	75	39
244	10	7795	7460	gi|467419	unknown [Bacillus subtilis]	75	56
247	1	7	1431	gi|577569	PepV [Lactobacillus delbrueckii]	75	54
250	5	3416	3201	gi|1580783	sperm receptor [Strongylocentrotus purpuratus]	75	50
256	1	2	562	gi|709991	hypothetical protein [Bacillus subtilis]	75	56
262	2	1031	2479	gi|142783	DNA photolyase [Bacillus firmus]	75	59
263	1	222	890	gi|148304	beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir|A42296|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790)	75	60
266	5	2224	1982	gnl|PID|e253211	ORF YDL065c [Saccharomyces cerevisiae]	75	50
269	2	1477	707	gi|1736647	ORF_ID:o347#4; similar to [SwissProt Accession Number P44634] [Escherichia coli]	75	61
276	11	7415	4593	gnl|PID|e221269	tail protein [Bacteriophage CP-1]	75	54
279	17	14992	14651	gi|1389549	ORF3 [Bacillus subtilis]	75	61
292	11	7829	8470	gi|160693	sporozoite surface protein [Plasmodium yoelii]	75	50
295	2	489	1157	gi|533099	endonuclease III [Bacillus subtilis]	75	59
307	4	3804	4889	gi|1321625	exo-alpha-1, 4-glucosidase [Bacillus stearothermophilus]	75	60
322	4	1088	1996	gi|310303	mosA [Rhizobium meliloti]	75	63
331	1	1	294	gi|1016092	ribosomal protein S14 [Cyanophora paradoxa]	75	57
334	7	6860	7969	gi|409286	bmrU [Bacillus subtilis]	75	45

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
340	1	3	743	gi|288413	glutamate dehydrogenase (NADP+) [Corynebacterium glutamicum] pir|S32227|S32227 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - orynebacterium glutamicum	75	60
343	2	1497	778	gi|46602	putative transposase (AA 1 - 224) [Staphylococcus aureus] ir|S12093|S12093 probable IS431mec protein - Staphylococcus aureus p|P19380|TRA2_STAAU TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT 431MEC.	75	54
372	3	865	1629	gi|146282	gut operon repressor (gutR) [Escherichia coli]	75	58
372	7	6614	5307	gnl|PID|e255128	trigger factor [Bacillus subtilis]	75	62
387	3	1721	1353	gi|580902	ORF6 gene product [Bacillus subtilis]	75	53
399	30	28774	29805	gi|146278	glucitol-specific enzyme II (gutA) [Escherichia coli] pir|A26725|WQEC2S phosphotransferase system enzyme II (EC .7.1.69), sorbitol-specific, factor II - Escherichia coli sp|P05705|PTHB_ECOLI PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC OMPONENT (EIIBC-GUT)	75	61
399	33	31077	32768	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	75	59
404	6	4994	4332	gi|1303921	YqiF [Bacillus subtilis]	75	64
404	7	4984	4829	gi|1303921	YqiF [Bacillus subtilis]	75	60
419	1	320	3	gi|496283	lysin [Bacteriophage Tuc2009]	75	67
431	3	1139	759	sp|P46351|YZGD_BACSU	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION.	75	60
473	1	166	2	gnl|PID|e229299	R04D3.8 [Caenorhabditis elegans]	75	35
481	1	1	351	gi|1573766	phosphoglyceromutase (gpmA) [Haemophilus influenzae]	75	64
492	1	440	3	gi|806487	ORF211; putative [Lactococcus lactis]	75	57

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
595	1	705	181	gi|147485	queA [Escherichia coli]	75	51
619	2	879	319	gi|1063246	low homology to P14 protein of Heamophilus influenzar and 14.2 kDa protein of Escherichia coli [Bacillus subtilis]	75	59
663	1	15	1544	gi|475112	enzyme IIabc [Pediococcus pentosaceus]	75	54
701	4	662	946	gi|143793	tyrosyl-tRNA synthetase [Bacillus caldotenax]	75	60
719	1	970	419	gi|727436	putative 20-kDa protein [Lactococcus lactis]	75	56
886	1	101	409	gi|143150	levR [Bacillus subtilis]	75	59
939	1	403	191	gi|425467	transposase [Lactobacillus helveticus]	75	53
984	2	66	227	gi|1652190	Fat protein [Synechocystis sp.]	75	48
17	2	2592	2924	gi|532556	ORF23 [Enterococcus faecalis]	74	53
17	25	24449	25639	gi|1458228	mutY homolog [Homo sapiens]	74	50
21	7	4729	5229	gi|726320	putative protein of unknown function encoded by the IS200-like lement [Yersinia pestis]	74	57
32	9	5819	4488	gi|1498962	M. jannaschii predicted coding region MJ0188 [Methanococcus jannaschii]	74	41
38	1	707	3	gi|142152	sulfate permease (gtg start codon) [Synechococcus PCC6301] pir|A30301|GRYCS7 sulfate transport protein - Synechococcus sp. PCC 7942)	74	53
44	1	1	927	gi|1377823	aminopeptidase [Bacillus subtilis]	74	63
60	8	8747	8070	gi|143368	phosphoribosylformyl glycinamidine synthetase I (PUR-L; gtg start odon) [Bacillus subtilis]	74	63
72	8	7388	7119	gnl|PID|e209004	glutaredoxin-like protein [Lactococcus lactis]	74	53
91	4	1031	2257	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis]	74	58
105	7	5553	5855	gi|467418	unknown [Bacillus subtilis]	74	63

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
110	18	16903	15842	gi|45288	arcB (AA 1-336) [Pseudomonas aeruginosa]	74	57
112	3	1112	636	gi|887824	ORF_o310 [Escherichia coli]	74	53
123	8	6105	7619	gi|1773191	similar to Pseudomonas sp. ORF5 [Escherichia coli]	74	60
128	1	2	1315	gi|143961	pyruvate phosphate dikinase [Clostridium symbiosum] pir|A36231|KIQAPO pyruvate,orthophosphate dikinase (EC 2.7.9.1) - lostridium symbiosum	74	58
128	26	18866	20401	gi|1303961	YqjJ [Bacillus subtilis]	74	57
150	5	4653	5303	gi|495046	tripeptidase [Lactococcus lactis]	74	53
159	8	7500	6850	gi|581098	GlnQ (AA 1-240); gtg start [Escherichia coli]	74	53
179	1	1259	57	gi|537080	ribonucleoside triphosphate reductase [Escherichia coli] pir|A47331|A47331 oxygen-sensitive ribonucleoside-triphosphate eductase (EC 1.17.4.-) - Escherichia coli	74	62
183	2	1669	224	gi|1146200	DNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis]	74	53
213	4	2265	3200	gi|1373157	orf-X; hypothetical protein; Method: conceptual translation supplied by author [Bacillus subtilis]	74	63
229	13	13774	12806	gnl|PID|e290288	Met-tRNAi formyl transferase [Bacillus subtilis]	74	55
238	31	28648	28052	gi|451072	di-tripeptide transporter [Lactococcus lactis]	74	56
244	8	6409	5552	gi|467422	unknown [Bacillus subtilis]	74	60
249	1	7	411	gi|1591758	diaminopimelate epimerase [Methanococcus jannaschii]	74	51
270	3	1832	3955	gi|1303829	YqfK [Bacillus subtilis]	74	55
276	3	1668	1357	gi|496282	holin [Bacteriophage Tuc2009]	74	54
288	9	5807	5076	gi|530063	glycerol uptake facilitator [Streptococcus	74	60

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

C ntig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					pneumoniae] sp|P52281|GLPF_STRPN GLYCEROL UPTAKE FACILITATOR PROTEIN.		
292	21	16780	17547	gi|1573646	Mg(2+) transport ATPase protein C (mgtC) (SP:P22037) [Haemophilus influenzae]	74	42
297	1	682	11	gnl|PID|e255093	hypothetical protein [Bacillus subtilis]	74	54
298	3	3562	3095	gi|1303970	YqjS [Bacillus subtilis]	74	46
321	10	5081	6028	pir|A32950|A32950	probable reductase protein - Leishmania major	74	56
327	2	904	3285	gi|1573876	virulence associated protein homolog (vacB) [Haemophilus influenzae]	74	53
334	5	3942	5432	gi|1652678	amidase [Synechocystis sp.]	74	57
341	13	13007	12069	gi|39881	ORF 311 (AA 1-311) [Bacillus subtilis]	74	53
362	7	3529	5274	gnl|PID|e255093	hypothetical protein [Bacillus subtilis]	74	58
376	3	1282	2346	gi|1773090	transfer RNA-guanine transglycosylase [Escherichia coli]	74	59
421	2	48	1400	gi|710632	beta-glucosidase [Bacillus subtilis]	74	58
471	1	815	3	gi|854234	cymG gene product [Klebsiella oxytoca]	74	53
480	2	263	607	gi|1303994	YqkM [Bacillus subtilis]	74	48
518	7	4409	5002	gi|145821	EBG enzyme alpha subunit [Escherichia coli]	74	47
539	8	6607	7179	gi|1165295	D3703.8p [Saccharomyces cerevisiae]	74	57
542	1	750	4	gi|1064810	function unknown [Bacillus subtilis]	74	56
559	1	1204	5	gi|43821	nifJ protein (AA 1-1171) [Klebsiella pneumoniae] p|P03833|NIFJ_KLEPN PYRUVATE-FLAVODOXIN OXIDOREDUCTASE (EC -.-.-).	74	58
579	3	1373	1624	gi|1237013	ORF2 [Bacillus subtilis]	74	46
624	4	2518	3669	gi|467394	recombination protein [Bacillus subtilis]	74	56
688	1	623	3	gi|662880	novel hemolytic factor [Bacillus cereus]	74	48
763	1	106	441	gi|153955	envM protein [Salmonella typhimurium]	74	46
811	1	3	158	gi|309662	pheromone binding protein [Plasmid pCF10]	74	57
852	1	2	601	gi|309662	pheromone binding protein [Plasmid pCF10]	74	53

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
935	1	976	2	gi|467403	seryl-tRNA synthetase [Bacillus subtilis]	74	59
22	2	2178	2471	gi|467460	unknown [Bacillus subtilis]	73	61
24	2	1126	3150	gi|1303822	YqfF [Bacillus subtilis]	73	54
33	6	6638	6970	gi|536971	ORF_o76 [Escherichia coli]	73	56
48	1	621	1241	gnl|PID|e274111	aggregation promoting protein [Lactobacillus gasseri]	73	67
48	6	5327	7225	gi|1185289	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacillus subtilis]	73	56
50	2	1097	2008	gi|1498295	homoserine kinase homolog [Streptococcus pneumoniae]	73	55
52	4	2793	4334	gi|473902	alpha-acetolactate synthase [Lactococcus lactis]	73	59
55	1	1	261	gi|396365	alternate name yjbA [Escherichia coli]	73	36
60	6	5935	5549	gi|551881	amidophosphoribosyltransferase [Lactobacillus casei] pir|PC1136|PC1136 purF protein - Lactobacillus casei (fragment) sp|P35853|PUR1_LACCA AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14) GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) FRAGMENT	73	57
74	2	477	1355	gnl|PID|e233567	unknown [Mycobacterium tuberculosis]	73	54
81	19	14213	13845	gi|606073	ORF_o169 [Escherichia coli]	73	52
93	7	2861	4075	gi|405134	acetate kinase [Bacillus subtilis]	73	56
100	1	1057	2	gi|1353561	ORF44 [Bacteriophage r1t]	73	52
100	41	28872	28627	gi|188492	heat shock-induced protein [Homo sapiens]	73	42
104	4	5558	5274	gi|312440	aspartate carbamoyltransferase [Bacillus caldolyticus] pir|S34318|S34318 aspartate carbamoyltransferase (EC 2.1.3.2) - acillus caldolyticus	73	55
119	5	3264	3638	gi|473707	positive regulator for virulence factors [Clostridium perfringens]	73	39

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
123	17	16156	15665	gi|1303703	YrkD [Bacillus subtilis]	73	37
123	18	16133	16465	gi|1303893	YqhL [Bacillus subtilis]	73	43
124	3	2165	1722	gi|486661	TMnm related protein [Saccharomyces cerevisiae]	73	45
127	6	5778	5101	gi|290561	o188 [Escherichia coli]	73	48
128	10	6896	7201	pir|S37387|S37387	internalin A precursor - Listeria monocytogenes	73	53
137	2	980	1954	gi|1276882	EpsI [Streptococcus thermophilus]	73	56
141	3	942	2777	gi|467336	unknown [Bacillus subtilis]	73	49
146	7	5611	4739	gi|149395	lacC [Lactococcus lactis]	73	56
154	6	3566	4621	gi|1354775	pfoS/R [Treponema pallidum]	73	46
155	8	7136	6726	gnl|PID|e247026	orf6 [Lactobacillus sake]	73	61
158	8	8693	7119	gi|1674275	(AE000056) Mycoplasma pneumoniae, hypothetical ABC transporter (yjcW) homolog; similar to Swiss-Prot Accession Number P32721, from E. coli [Mycoplasma pneumoniae]	73	45
162	4	4039	3305	gi|142997	glycerol uptake facilitator [Bacillus subtilis]	73	55
165	4	3962	3105	gi|882736	ORF_f278 [Escherichia coli]	73	58
171	3	3952	4689	gnl|PID|e63527	FtsE [Mycobacterium tuberculosis]	73	56
171	5	5673	6596	gi|1303854	YqgG [Bacillus subtilis]	73	59
179	9	9302	10414	gnl|PID|e254984	hypothetical protein [Bacillus subtilis]	73	55
180	1	24	1151	gi|43985	nifS-like gene [Lactobacillus delbrueckii]	73	56
181	12	10036	9674	gnl|PID|e220317	chorismate mutase [Staphylococcus xylosus]	73	50
181	13	10713	10003	gi|39813	phospho-2-dehydro-3-deoxyheptonate aldolase [Bacillus subtilis] ir|S21418|S21418 phospho-2-dehydro-3-deoxyheptonate aldolase (EC 1.2.15) - Bacillus subtilis	73	56
183	3	2716	1667	gi|1146199	putative [Bacillus subtilis]	73	36

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
198	1	869	108	gi|142854	homologous to E. coli radC gene product and to unidentified protein rom Staphylococcus aureus [Bacillus subtilis]	73	47
210	1	956	3	gnl|PID|e281310	acetyl coenzyme A acetyltransferase (thiolase) [Thermoanaerobacterium thermosaccharolyticum]	73	54
230	1	1	171	gi|304143	S-layer protein [Bacillus circulans]	73	46
235	1	715	2	gi|1732315	transport system permease homolog [Listeria monocytogenes]	73	49
235	2	888	676	gi|551726	sporulation protein [Bacillus subtilis]	73	54
242	4	3290	3517	gnl|PID|e236570	orf6 gene product [Enterococcus faecalis]	73	30
242	8	5914	6492	gi|1742340	HipB protein. [Escherichia coli]	73	49
250	3	3037	2411	gi|1174238	TipB [Pseudomonas fluorescens]	73	57
254	5	1124	792	gi|580900	ORF3 gene product [Bacillus subtilis]	73	52
269	9	5507	5154	gi|1303790	YqeI [Bacillus subtilis]	73	60
269	12	7989	7345	gi|285621	undefined open reading frame [Bacillus stearothermophilus]	73	54
284	1	1	915	gi|455528	ORF2 [Streptococcus thermophilus bacteriophage]	73	54
290	3	1932	2678	gnl|PID|e248883	unknown [Mycobacterium tuberculosis]	73	57
295	8	4521	4739	gi|145478	putative [Escherichia coli]	73	56
296	1	2	1846	gnl|PID|e249642	transketolase [Bacillus subtilis]	73	59
310	4	3488	3036	gi|1591900	nucleoside diphosphate kinase [Methanococcus jannaschii]	73	48
313	1	17	778	gi|1658371	cyclic beta-1,2-glucan modification protein [Rhizobium meliloti]	73	60
314	3	2642	2067	gi|1330343	C34D4.12 gene product [Caenorhabditis elegans]	73	56
325	1	492	4	gi|407908	EIIscr [Staphylococcus xylosus]	73	56
345	19	20549	21901	gi|443691	glutathione reductase [Streptococcus thermophilus]	73	59

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
359	4	3280	2252	gi|1001478	hypothetical protein [Synechocystis sp.]	73	50
374	1	884	3	gi|435123	PacL [Synechococcus sp.]	73	58
379	6	5676	4339	gi|887822	possible frameshift at end to join to next ORF? [Escherichia coli]	73	57
383	4	3815	3387	gi|1651732	mutator MutT protein [Synechocystis sp.]	73	52
392	4	3454	5202	gi|294587	minimal change nephritis transmembrane glycoprotein [Rattus orvegicus]	73	56
394	5	4267	5250	gi|49011	amidinotransferase II [Streptomyces griseus]	73	42
395	10	4252	4608	gi|1591139	M. jannaschii predicted coding region MJ0435 [Methanococcus jannaschii]	73	48
397	1	885	4	gnl|PID|e249658	GrlA [Bacillus subtilis]	73	56
399	15	10007	11569	gi|565619	citrate lyase alpha-subunit [Klebsiella pneumoniae] pir|S60776|S60776 citrate (pro-3S)-lyase (EC 4.1.3.6) alpha chain - lebsiella pneumoniae	73	54
416	2	660	1649	gi|475114	regulatory protein [Pediococcus pentosaceus]	73	50
436	6	4124	3540	gi|727436	putative 20-kDa protein [Lactococcus lactis]	73	53
446	3	1618	4260	gi|882711	exonuclease V alpha-subunit [Escherichia coli]	73	48
462	1	819	43	gi|1399011	immunogenic secreted protein precursor [Streptococcus pyogenes]	73	63
482	5	3181	2501	gi|1072419	glcB gene product [Staphylococcus carnosus]	73	55
495	4	1340	3031	gi|146547	kdpA [Escherichia coli]	73	55
523	4	2354	1821	pir|A00392|RDSODF	dihydrofolate reductase (EC 1.5.1.3) - Enterococcus faecium	73	54
543	5	3099	2893	gi|19743	nsGRP-2 [Nicotiana sylvestris]	73	53
567	1	9	740	gi|1147601	cyclophilin isoform 4 [Caenorhabditis elegans]	73	54

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
629	1	945	4	gi|1006620	ABC transporter [Synechocystis sp.]	73	46
714	2	344	556	gi|1045872	ATP-binding protein [Mycoplasma genitalium]	73	61
747	1	320	3	gi|437389	transposase [Lactococcus lactis]	73	56
764	1	3	515	gi|532554	ORF21 [Enterococcus faecalis]	73	50
766	1	683	3	gi|1673788	(AE000015) Mycoplasma pneumoniae, fructose-bisphosphate aldolase; similar to Swiss-Prot Accession Number P13243, from B. subtilis [Mycoplasma pneumoniae]	73	52
880	1	198	4	gi|309661	regulatory protein [Plasmid pCF10]	73	50
897	1	3	170	gi|807976	unknown [Saccharomyces cerevisiae]	73	57
5	1	223	2	gnl|PID|e255315	unknown [Mycobacterium tuberculosis]	72	56
8	5	4158	4799	gi|587088	shikimate kinase [Bacillus subtilis]	72	54
19	6	2600	2833	gi|34844	embryonic myosin heavy chain (AA 1 - 1940) [Homo sapiens] ir|S04090|S04090 myosin heavy chain, skeletal muscle, embryonic - man	72	38
19	25	12872	14605	gnl|PID|e242896	orf5 [Bacteriophage A2]	72	52
21	4	2777	2598	gi|54115	skeletal muscle chloride channel [Mus musculus domesticus]	72	45
23	7	3702	4847	gi|144714	NADPH-dependent butanol dehydrogenase [Clostridium acetobutylicum] pir|JU0053|JU0053 NADPH-dependent butanol dehydrogenase - lostridium acetobutylicum	72	48
32	1	1073	3	gi|1303839	YqfR [Bacillus subtilis]	72	50
39	8	4137	3244	pir|A32950|A32950	probable reductase protein - Leishmania major	72	55
43	3	969	1919	gi|290494	o287 [Escherichia coli]	72	46
45	2	911	1567	gi|1039479	ORFU [Lactococcus lactis]	72	50
55	6	2549	2896	gi|755602	unknown [Bacillus subtilis]	72	51
55	7	3178	3660	gi|1303914	YqhY [Bacillus subtilis]	72	49

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
60	1	1302	34	gi|143374	phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) Bacillus subtilis]	72	59
60	3	3422	2838	gi|143372	phosphoribosyl glycinamide formyltransferase (PUR-N) [Bacillus ubtilis]	72	48
60	10	9771	9010	gi|143367	phosphoribosyl aminoidazole succinocarboxamide synthetase (PUR-C; tg start codon) [Bacillus subtilis]	72	57
70	5	3615	3833	sp|P43672|YCBH_ECOLI	HYPOTHETICAL 14.4 KD PROTEIN IN PYRD-PQIA INTERGENIC REGION.	72	48
79	2	632	841	gi|1652343	ABC transporter [Synechocystis sp.]	72	47
85	2	1843	770	gi|1354775	pfoS/R [Treponema pallidum]	72	45
87	1	2	745	gi|42029	ORF1 gene product [Escherichia coli]	72	47
88	1	124	1047	gi|535348	CodV [Bacillus subtilis]	72	50
88	7	3862	4752	gi|149413	ORF [Lactococcus lactis]	72	51
91	2	611	877	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis]	72	57
98	16	16302	15163	gi|147326	transport protein [Escherichia coli]	72	57
101	6	4676	4023	gi|1109685	ProW [Bacillus subtilis]	72	53
104	3	5331	3982	gi|312441	dihydroorotase [Bacillus caldolyticus]	72	58
114	10	11165	12205	gi|556881	Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis] pir|S49358|S49358 ipc-29d protein - Bacillus subtilis sp|P39153|YWLC_BACSU HYPOTHETICAL 37.0 KD PROTEIN IN SPOIIR-GLYC NTERGENIC REGION.	72	60
128	19	14325	11560	gi|143150	levR [Bacillus subtilis]	72	58
130	2	382	1437	gi|308850	ATP binding protein [Lactococcus lactis]	72	55
135	4	5012	3693	gi|413940	ipa-16d gene product [Bacillus subtilis]	72	56
150	6	5114	5878	gi|495046	tripeptidase [Lactococcus lactis]	72	54
154	9	5850	5677	gi|425467	transposase [Lactobacillus helveticus]	72	52

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
168	4	1375	1563	gi|1652869	NADH dehydrogenase [Synechocystis sp.]	72	55
173	5	2879	4024	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	72	57
179	2	1608	2399	gi|709993	hypothetical protein [Bacillus subtilis]	72	45
179	6	7584	7844	gi|1161934	DltC [Lactobacillus casei]	72	54
180	21	19948	21105	gi|1773197	similar to M. fervidus malate dehydrogenase [Escherichia coli]	72	55
182	1	3	413	gi|1146182	putative [Bacillus subtilis]	72	48
200	23	13106	12789	gi|1707358	polyprotein precurser [Soybean mosaic virus]	72	34
204	6	2462	2289	gi|1200525	dihydrolipoamide acetyltransferase [Pseudomonas aeruginosa]	72	61
204	9	6374	5187	gi|1732040	alcohol dehydrogenase [Actinobacillus pleuropneumoniae]	72	56
205	1	463	71	gi|42029	ORF1 gene product [Escherichia coli]	72	57
210	7	6433	5279	gi|142978	glycerol dehydrogenase [Bacillus stearothermophilus] pir|JQ1474|JQ1474 glycerol dehydrogenase (EC 1.1.1.6) - Bacillus tearothermophilus	72	46
213	6	4086	5141	gi|431231	uracil permease [Bacillus caldolyticus]	72	51
223	1	99	833	gi|1573615	ATP-binding protein (abc) [Haemophilus influenzae]	72	47
227	1	26	886	gi|1070015	protein-dependent [Bacillus subtilis]	72	52
228	4	2047	2481	gi|467339	unknown [Bacillus subtilis]	72	50
238	17	14728	15582	gi|882736	ORF_f278 [Escherichia coli]	72	59
250	6	4169	4765	gi|437389	transposase [Lactococcus lactis]	72	56
258	7	5296	7089	gi|192185	acid beta-galactosidase [Mus musculus]	72	53
266	3	2024	1773	gi|145149	ORFd [Escherichia coli]	72	50
269	8	5142	4477	gi|1303791	YqeJ [Bacillus subtilis]	72	45
276	13	9843	8152	gnl|PID|e59644	predicted 86.4kd protein; 52Kd observed [Mycobacteriophage 15]	72	48
278	2	965	1573	gi|425467	transposase [Lactobacillus helveticus]	72	52

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
279	2	1305	340	gnl|PID|e198981	ttg start [Campylobacter coli]	72	47
283	4	1668	2045	gi|1353563	ORF46 [Bacteriophage r1t]	72	48
286	2	789	2606	gi|1651216	Pz-peptidase [Bacillus licheniformis]	72	52
290	4	2676	3239	gi|1653645	ribosome releasing factor [Synechocystis sp.]	72	56
301	2	1762	899	gi|606013	CG Site No. 829 [Escherichia coli]	72	57
362	2	377	688	gi|1001826	cadmium-transporting ATPase [Synechocystis sp.]	72	53
369	1	582	142	gi|153745	mannitol-specific enzyme III [Streptococcus mutans] pir|B44798|B44798 mannitol-specific factor III, MtlF - treptococcus mutans	72	47
379	2	1934	1527	gi|1055071	C23G10.2 gene product [Caenorhabditis elegans]	72	51
384	2	694	1098	gi|1208474	hypothetical protein [Synechocystis sp.]	72	49
388	1	291	4	gi|1673836	(AE000018) Mycoplasma pneumoniae, osmotically inducible protein; similar to Swiss-Prot Accession Number P23929, from E. coli [Mycoplasma pneumoniae]	72	43
401	6	3995	5137	gi|508242	ORF 6, putative Galf synthesis pathway protein [Escherichia coli] gi|510253 orf6 [Escherichia coli]	72	62
404	2	2119	776	gi|466474	cellobiose phosphotransferase enzyme II'' [Bacillus tearothermophilus]	72	48
416	4	3461	1980	gi|710632	beta-glucosidase [Bacillus subtilis]	72	55
416	7	6285	5551	gnl|PID|e269549	Unknown [Bacillus subtilis]	72	52
419	3	759	505	gi|928830	ORF75; putative [Lactococcus lactis phage BK5-T]	72	47
441	4	3420	4676	gi|1732195	beta-cystathionase [Vibrio furnissii]	72	54
460	3	1385	2641	gi|1652389	beta ketoacyl-acyl carrier protein synthase [Synechocystis sp.]	72	55
460	5	3129	3560	gnl|PID|e289141	similar to hydroxymyristoyl-(acyl carrier	72	54

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					protein) dehydratase [Bacillus subtilis]		
460	8	5817	6023	gi|285621	undefined open reading frame [Bacillus stearothermophilus]	72	57
462	2	1591	785	gi|148304	beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir|A42296|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790)	72	51
467	1	2	706	gi|148711	6-aminohexanoate-cyclic-dimer hydrolase [Flavobacterium sp.] gi|488343 6-aminohexanoate-cyclic-dimer hydrolase [Flavobacterium p.]	72	50
469	3	1144	1419	gi|466474	cellobiose phosphotransferase enzyme II'' [Bacillus tearothermophilus]	72	48
493	1	1124	240	sp|P50848|YPWA_BACSU	HYPOTHETICAL 58.2 KD PROTEIN IN KDGT-XPT INTERGENIC REGION.	72	58
536	2	379	218	gi|437389	transposase [Lactococcus lactis]	72	58
543	1	574	86	gi|290513	f470 [Escherichia coli]	72	47
592	1	57	680	gi|987092	ABC-transporter [Streptomyces hygroscopicus]	72	55
666	2	551	967	gi|1064786	function unknown [Bacillus subtilis]	72	48
762	1	974	273	gi|304928	pantothenate synthetase [Escherichia coli]	72	55
792	1	401	3	pir|A36933|A36933	diacylglycerol kinase homolog - Streptococcus mutans	72	50
873	1	183	4	gnl|PID|e258329	oxaloacetate decarboxylase alpha-chain [Legionella pneumophila]	72	55
4	4	3799	3155	gi|496943	ORF [Saccharomyces cerevisiae]	71	45
10	2	180	977	gnl|PID|e234078	hom [Lactococcus lactis]	71	49
16	7	4922	6097	gi|534982	phosphoglucomutase [Spinacia oleracea]	71	54
21	6	4148	3972	gi|1736645	Proline/betaine transporter (Proline porter II) (PPII). [Escherichia coli]	71	50
23	27	16452	17459	gi|1408503	yxeR gene product [Bacillus subtilis]	71	52
25	7	5812	6669	gi|413943	ipa-19d gene product [Bacillus subtilis]	71	58

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
31	1	80	946	gi|534045	antiterminator [Bacillus subtilis]	71	47
39	3	755	1297	sp|P09997|YIDA_ECOLI	HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION.	71	50
39	7	2537	3193	pir|C43748|C43748	hypothetical protein (pepX 3' region) - Lactococcus lactis subsp. lactis	71	54
45	10	5119	5484	gi|606044	ORF_o130; Geneplot suggests frameshift, none found [Escherichia oli]	71	51
48	10	11722	10148	gi|20432	4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544) [Petroselinum crispum] ir|S01667|S01667 4-coumarate--CoA ligase (EC 6.2.1.12) (clone 4CL-1) - parsley	71	39
55	4	1470	1709	gi|1303901	YqhT [Bacillus subtilis]	71	54
57	10	12899	13060	gi|40053	phenylalanyl-tRNA synthetase alpha subunit [Bacillus subtilis] ir|S11730|YFBSA phenylalanine--tRNA ligase (EC 6.1.1.20) alpha ain - Bacillus subtilis	71	45
58	3	3743	2571	gi|1658403	formate dehydrogenase alpha subunit [Moorella thermoacetica]	71	51
68	11	8225	8602	gi|793910	surface antigen [Homo sapiens]	71	49
74	4	2908	2042	gi|467435	unknown [Bacillus subtilis]	71	55
85	3	3267	1966	gi|142613	branched chain alpha-keto acid dehydrogenase E2 [Bacillus subtilis] gi|1303944 BfmBB [Bacillus subtilis]	71	56
111	8	5737	4253	gi|1256135	YbbF [Bacillus subtilis]	71	50
111	9	6590	5730	gi|1573762	glucokinase regulator [Haemophilus influenzae]	71	53
120	1	111	353	gnl|PID|e235823	unknown [Schizosaccharomyces pombe]	71	52
123	11	10387	11196	gi|1773195	hypothetical [Escherichia coli]	71	55
151	3	4045	3098	gi|1256618	transport protein [Bacillus subtilis]	71	51
172	6	3949	4806	gi|1262288	CdsA [Brucella abortus]	71	56
172	7	5264	6448	gi|40100	rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir|S06049|S06049 rodC	71	52

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					protein - Bacillus subtilis p|P13485|TAGF_BACSU TEICHOIC ACID BIOSYNTHESIS PROTEIN F.		
190	7	3454	3122	gi|532556	ORF23 [Enterococcus faecalis]	71	52
195	24	9850	11871	gi|405564	traE [Plasmid pSK41]	71	45
215	4	3361	2711	gi|1573086	uridine kinase (uridine monophosphokinase) (udk) [Haemophilus influenzae]	71	51
218	2	1456	2613	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	71	41
222	3	1205	2053	gnl|PID|e255114	glutamate racemase [Bacillus subtilis]	71	56
222	4	1611	1387	gi|1001195	phosphate transport system permease protein PstA [Synechocystis sp.]	71	57
222	14	8852	9853	gi|466720	No definition line found [Escherichia coli]	71	53
238	22	19256	20578	gi|595299	YgiK [Salmonella typhimurium]	71	50
255	3	2692	1061	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	71	55
265	5	2960	1581	gi|1039479	ORFU [Lactococcus lactis]	71	58
276	2	1359	538	gi|496283	lysin [Bacteriophage Tuc2009]	71	63
290	5	3552	4379	gi|1016162	ABC transporter subunit [Cyanophora paradoxa]	71	49
290	7	5659	6912	gi|1001708	NifS [Synechocystis sp.]	71	56
292	3	948	2156	gnl|PID|e233874	hypothetical protein [Bacillus subtilis]	71	55
318	4	3229	2285	gi|1256138	YbbI [Bacillus subtilis]	71	54
333	1	145	741	gi|293011	unknown protein [Lactococcus lactis]	71	50
344	1	76	396	gi|853775	unknown [Bacillus subtilis]	71	53
350	1	138	1394	gi|1652389	beta ketoacyl-acyl carrier protein synthase [Synechocystis sp.]	71	57
363	4	4184	5674	gi|1657518	similar to fdrA gene of E. coli [Escherichia coli]	71	54
364	5	5319	6563	gi|1657522	hypothetical protein [Escherichia coli]	71	46
367	13	6539	6162	gi|44225	ribosomal protein L18 (AA 1-116)	71	51

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Mycoplasma capricolum] ir|S02847|R5YM18 ribosomal protein L18 - Mycoplasma capricolum GC3)		
379	7	6884	5655	gi|887821	ORF_o398 [Escherichia coli]	71	50
399	9	6528	7664	gi|154198	oxaloacetate decarboxylase [Salmonella typhimurium] pir|C44465|C44465 sodium ion pump oxaloacetate decarboxylase ubunit beta - Salmonella typhimurium	71	50
399	18	13540	14778	gi|143165	malic enzyme (EC 1.1.1.38) [Bacillus stearothermophilus] pir|A33307|DEBSXS malate dehydrogenase oxaloacetate-decarboxylating) (EC 1.1.1.38) - Bacillus tearothermophilus	71	46
404	4	3769	3029	gi|143402	recombination protein (ttg start codon) [Bacillus subtilis] gi|1303923 RecN [Bacillus subtilis]	71	48
464	1	1532	216	gi|895749	putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis]	71	40
464	3	2088	2846	gi|1486242	unknown [Bacillus subtilis]	71	39
481	2	954	409	gi|144729	butanol dehydrogenase [Clostridium acetobutylicum] sp|Q04944|ADHA_CLOAB NADH-DEPENDENT BUTANOL DEHYDROGENASE A (EC .1.1.-) (BDH I).	71	58
482	4	2503	1841	gi|1072418	glcA gene product [Staphylococcus carnosus]	71	58
496	2	1636	848	gi|1001226	methionine aminopeptidase [Synechocystis sp.]	71	51
503	2	1624	650	gi|39478	ATP binding protein of transport ATPases [Bacillus firmus] ir|S15486|S15486 ATP-binding protein - Bacillus firmus p|P26946|YATR_BACFI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING OTEIN.	71	49

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

C ntig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
513	2	1590	982	gnl|PID|e202290	unknown [Lactobacillus sake]	71	46
530	1	2	1534	gi|1542974	AbcA [Thermoanaerobacterium thermosulfurigenes]	71	52
537	1	706	365	gi|929972	ORFB; similar to B. anthracis SterneL element ORFB; putative S150-like transposase [Bacillus anthracis]	71	57
553	1	304	1287	gi|1653479	regulatory components of sensory transduction system [Synechocystis sp.]	71	48
573	9	5560	5090	gi|143799	MtrA [Bacillus subtilis]	71	59
583	1	21	341	gi|1064791	function umknown [Bacillus subtilis]	71	50
584	2	638	276	gi|662792	single-stranded DNA binding protein [unidentified eubacterium]	71	58
585	1	282	809	gi|666972	ORF 168 [Synechococcus sp.]	71	46
611	1	985	2	gi|1039479	ORFU [Lactococcus lactis]	71	55
616	1	350	3	gi|1088272	nitrogen fixation protein [Bacillus cereus]	71	52
624	1	61	399	gi|40014	pot. ORF 446 (aa 1-446) [Bacillus subtilis]	71	53
624	2	608	1732	gi|40015	pot. ORF 378 (aa 1-378) [Bacillus subtilis]	71	51
659	1	76	582	gi|1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	71	51
668	2	836	1030	gi|467330	replicative DNA helicase [Bacillus subtilis]	71	60
683	1	582	118	gnl|PID|e264663	CinA [Streptococcus pneumoniae]	71	55
701	3	411	797	gi|143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	71	51
720	1	1	351	gi|1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	71	55
724	2	1020	415	gnl|PID|e239621	ORF YNL218w [Saccharomyces cerevisiae]	71	51
790	2	658	383	gi|1783253	homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis]	71	48

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
799	1	505	906	gi|580866	ipa-12d gene product [Bacillus subtilis]	71	45
974	2	139	333	gi|1778531	HI0021 homolog [Escherichia coli]	71	42
980	1	156	497	gi|437389	transposase [Lactococcus lactis]	71	57
4	3	3170	2418	gi|1001805	hypothetical protein [Synechocystis sp.]	70	55
17	21	18642	21527	gi|145821	EBG enzyme alpha subunit [Escherichia coli]	70	53
19	8	2894	3952	gi|1353527	ORF10 [Bacteriophage r1t]	70	58
23	6	2640	3230	gi|699336	C. freundii orfW homologue [Mycobacterium leprae] sp|P53523|Y02Y_MYCLE HYPOTHETICAL 20.9 KD PROTEIN U471A.	70	43
27	3	1011	493	gi|1001644	regulatory components of sensory transduction system [Synechocystis sp.]	70	44
31	2	1095	1337	gi|1100076	PTS-dependent enzyme II [Clostridium longisporum]	70	55
32	10	6527	5817	gi|1591789	M. jannaschii predicted coding region MJ1163 [Methanococcus jannaschii]	70	51
33	7	6930	7235	gi|536972	ORF_o90a [Escherichia coli]	70	45
35	2	500	2533	gi|43819	nagE gene product [Klebsiella pneumoniae]	70	50
47	13	15837	14512	gi|150209	ORF 1 [Mycoplasma mycoides]	70	44
49	15	10409	11179	gi|853751	N-acetylmuramoyl-L-alanine amidase [Bacteriophage A511]	70	54
57	7	8365	12189	gi|142440	ATP-dependent nuclease [Bacillus subtilis]	70	48
57	16	18656	18033	gi|388565	major cell-binding factor [Campylobacter jejuni]	70	52
59	9	4985	7060	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	70	49
72	6	6771	4600	gi|557567	ribonucleotide reductase R1 subunit [Mycobacterium tuberculosis] sp|P50640|RIR1_MYCTU RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA HAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) (R1 SUBUNIT) FRAGMENT).	70	53
76	8	5960	6343	gi|1063251	no homologous protein [Bacillus subtilis]	70	52

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
81	16	12529	11723	gi|1732200	PTS permease for mannose subunit IIPMan [Vibrio furnissii]	70	52
98	7	8974	7874	gi|1573045	hypothetical [Haemophilus influenzae]	70	46
110	2	1353	502	gi|1399848	unknown [Synechococcus PCC7942]	70	52
123	7	5009	5527	gi|143284	negative regulator pai 1 [Bacillus subtilis]	70	51
123	22	19729	20412	gi|1591493	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	70	48
133	6	5905	6498	gi|746399	transcription elongation factor [Escherichia coli]	70	50
134	1	1	384	gi|1146242	aspartate 1-decarboxylase [Bacillus subtilis]	70	49
138	10	8543	7953	gi|467371	LACI family of transcriptional repreesor (probable) [Bacillus ubtilis]	70	50
160	3	1263	1520	gi|1468939	meso-2,3-butanediol dehydrogenase (D-acetoin forming) [Klebsiella pneumoniae]	70	45
174	3	2279	1572	gi|413931	ipa-7d gene product [Bacillus subtilis]	70	44
177	2	2104	1022	gnl|PID|e186242	D-mannonate hydrolase [Thermotoga neapolitana]	70	52
178	2	1320	532	gi|499659	K+ channel protein [Panulirus interruptus]	70	51
180	18	17770	18729	gi|887824	ORF_o310 [Escherichia coli]	70	50
180	22	21072	22526	gi|1573294	hypothetical [Haemophilus influenzae]	70	40
181	9	7409	6279	sp|P20692|TYRA_BACSU	PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).	70	49
197	5	4529	6340	gi|1783252	homologous to many ATP-binding transport proteins including SwissProt:CYDD_ECOLI; hypothetical [Bacillus subtilis]	70	47
200	21	12419	11820	gi|290943	HindIII modification methyltransferase [Haemophilus influenzae] sp|P43871|MTH3_HAEIN MODIFICATION METHYLASE HINDIII (EC 2.1.1.72) ADENINE-SPECIFIC METHYLTRANSFERASE HINDIII)	70	47

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					(M.HINDIII).		
210	4	3877	3269	gi|602683	orfC [Mycoplasma capricolum]	70	47
217	2	405	707	gi|153767	ORF [Streptococcus pneumoniae]	70	56
222	8	4940	6046	gi|537033	ORF_f356 [Escherichia coli]	70	54
222	15	9825	10553	gi|537039	ORF_o228a [Escherichia coli]	70	56
227	4	1871	2893	gi|1070014	protein-dependent [Bacillus subtilis]	70	44
228	2	1343	792	gi|1742730	Protein AraJ precursor. [Escherichia coli]	70	50
228	5	3470	2574	gi|1573390	hypothetical [Haemophilus influenzae]	70	54
231	2	2470	1238	gi|1574085	H. influenzae predicted coding region HI1048 [Haemophilus influenzae]	70	48
235	4	2779	2138	gi|309662	pheromone binding protein [Plasmid pCF10]	70	46
239	4	5807	6409	gi|682765	mccB gene product [Escherichia coli]	70	41
248	1	3	350	gi|143725	putative [Bacillus subtilis]	70	52
254	4	838	497	gi|49318	ORF4 gene product [Bacillus subtilis]	70	48
256	3	1737	2612	gi|596092	putative multiple membrane domain protein; possible TTG initiation odon at position 1064, near putative RBS at position 1052 Streptococcus pyogenes]	70	51
279	15	14547	14224	gi|1389549	ORF3 [Bacillus subtilis]	70	50
283	6	2279	3190	gi|853751	N-acetylmuramoyl-L-alanine amidase [Bacteriophage A511]	70	52
292	8	5557	6534	gi|474195	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB ' region from E. coli, Accession Number X61000 [Mycoplasma-like rganism]	70	50
294	8	2776	3375	gi|1750126	YncB [Bacillus subtilis]	70	47
294	10	3742	4020	gi|984581	YafQ [Escherichia coli]	70	50
299	1	905	132	gi|606309	ORF_o265; gtg start [Escherichia coli]	70	40
300	3	3200	2784	gi|289260	comE ORF1 [Bacillus subtilis]	70	50
301	9	8564	7590	gi|1303865	YqgR [Bacillus subtilis]	70	52
336	2	661	921	gi|202864	[Rat alternatively spliced mRNA.], gene	70	47

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					product [Rattus norvegicus]		
339	1	269	3	gi|786163	Ribosomal Protein L10 [Bacillus subtilis]	70	50
351	9	4760	4359	gi|799235	dTDP-6-deoxy-L-lyxo-4-hexulose reductase [Escherichia coli]	70	45
399	28	28203	28793	gi|146278	glucitol-specific enzyme II (gutA) [Escherichia coli] pir|A26725|WQEC2S phosphotransferase system enzyme II (EC .7.1.69), sorbitol-specific, factor II - Escherichia coli sp|P05705|PTHB_ECOLI PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC OMPONENT (EIIBC-GUT)	70	52
406	1	1	552	gi|49315	ORF1 gene product [Bacillus subtilis]	70	50
436	5	2417	2193	gi|773665	transposase [Lactococcus lactis]	70	36
482	3	1887	1660	gi|48680	ptsG-like product [Bacillus subtilis]	70	47
529	3	6587	7030	gi|1022726	unknown [Staphylococcus haemolyticus]	70	44
535	2	1702	965	gi|1747435	KdpE [Clostridium acetobutylicum]	70	52
543	2	1248	547	gi|1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	70	47
543	8	4084	3878	gi|511976	SERP gene gene product [Plasmodium falciparum]	70	60
560	3	1037	876	gi|558458	acidic 82 kDa protein [Homo sapiens]	70	40
573	4	1920	2258	gi|336639	prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] gi|1016130 prenyl transferase [Cyanophora paradoxa] pir|A40433|A40433 prephytoene pyrophosphatase dehydrogenase (crtE) omolog - Cyanophora paradoxa	70	32
599	2	244	573	gi|42029	ORF1 gene product [Escherichia coli]	70	49
608	3	867	556	gi|475032	formamidopyrimidine-DNA glycosylase [Streptococcus mutans] sp|P55045|FPG_STRMU FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC .2.2.23) (FAPY-DNA GLYCOSYLASE).	70	53

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
636	1	2	628	gi|606309	ORF_o265; gtg start [Escherichia coli]	70	50
670	2	2157	1828	gi|1657698	hyaluronan receptor [Homo sapiens]	70	41
702	1	103	870	gi|149490	sucrose-6-phosphate hydrolase [Lactococcus lactis] pir|JH0754|JH0754 sucrose-6-phosphate hydrolase (EC 3.2.1.-) - actococcus lactis	70	51
726	2	725	480	gnl|PID|e240103	unknown ORF [Saccharomyces cerevisiae]	70	41
854	1	1	207	gi|532653	thermonuclease [Staphylococcus hyicus]	70	51
901	1	238	447	gi|172022	myosin 1 isoform (MYO2) [Saccharomyces cerevisiae]	70	20
940	1	1	318	gi|1039479	ORFU [Lactococcus lactis]	70	56
1	2	2112	1213	gi|413976	ipa-52r gene product [Bacillus subtilis]	69	51
8	2	2196	778	gi|1510108	ORF-1 [Agrobacterium tumefaciens]	69	50
8	9	7949	6654	gi|1196907	daunorubicin resistance protein [Streptomyces peucetius]	69	44
16	3	1618	2574	gi|1109684	ProV [Bacillus subtilis]	69	53
17	26	25781	26944	gi|485275	53.6 kDa protein [Streptococcus pneumoniae]	69	44
17	35	32300	32770	gi|1574146	pfs protein (pfs) [Haemophilus influenzae]	69	53
23	30	18107	18538	gnl|PID|e249656	YneT [Bacillus subtilis]	69	59
25	8	6653	6994	gi|413943	ipa-19d gene product [Bacillus subtilis]	69	46
37	2	2042	186	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	69	52
39	2	528	767	gi|1408493	homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	69	52
56	6	4809	3457	gi|1591610	probable ATP-dependent helicase [Methanococcus jannaschii]	69	45
67	5	3042	3938	gi|1658188	oxidative stress transcriptional regulator	69	39

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Erwinia carotovora]		
68	3	684	1529	gnl|PID|e214719	PlcR protein [Bacillus thuringiensis]	69	45
72	4	2099	3394	gi|882672	ORF_o313 [Escherichia coli]	69	37
81	15	11820	10915	gi|1732201	PTS permease for mannose subunit IIBMan [Vibrio furnissii]	69	44
83	20	14001	15800	gi|1230668	Similar to Arginyl-tRNA synthetase (Swiss Prot. accession number P11875) [Saccharomyces cerevisiae]	69	44
85	6	6309	5299	sp|P54533|DLD2_BACSU	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4) (DIHYDROLIPOAMIDE DEHYDROGENASE) (LPD-VAL).	69	46
86	3	2084	3367	gi|143318	phosphoglycerate kinase [Bacillus megaterium]	69	53
94	2	1401	751	gi|755216	N-acetylmuramidase [Lactococcus lactis]	69	41
94	16	20498	19197	gi|1208948	unknown [Escherichia coli]	69	47
98	8	10201	9029	gi|563934	similar to E. coli hypothetical protein: PIR Accession Number Q0614] [Bacillus subtilis]	69	51
109	4	2350	1316	gi|396501	aspartyl-tRNA synthetase [Thermus aquaticus thermophilus] pir|S33743|S33743 aspartate--tRNA ligase (EC 6.1.1.12) - Thermus quaticus	69	56
114	1	83	1522	gi|1658402	formate dehydrogenase beta subunit [Moorella thermoacetica]	69	45
123	9	7617	8984	gi|1773192	similar to S. cerevisiae dal1 [Escherichia coli]	69	50
128	11	7940	7578	gi|895750	putative cellobiose phosphotransferase enzyme III [Bacillus ubtilis]	69	53
130	10	8764	9036	gi|1641	put. Na(+)/glucose co-transporter (AA 1-662) [Oryctolagus cuniculus] |1717	69	47

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					cortical sodium-D-glucose cotransporter [Oryctolagus iculus]		
138	26	16721	17545	pir|A25805|A25805	L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis	69	55
139	2	310	1083	gi|1408587	relaxase [Lactococcus lactis lactis]	69	46
139	9	5196	4984	gi|473955	DNA-binding protein [Lactobacillus sp.]	69	34
142	9	5559	4564	gi|623073	ORF360; putative [Bacteriophage LL-H]	69	47
155	6	4658	5818	gi|1591260	endoglucanase [Methanococcus jannaschii]	69	48
158	12	11671	11201	gi|606744	cytidine deaminase [Bacillus subtilis]	69	52
162	5	5888	4032	gi|142993	glycerol-3-phosphate dehydrogenase (glpD) (EC 1.1.99.5) [Bacillus ubtilis]	69	54
180	2	1901	1203	gi|1575577	DNA-binding response regulator [Thermotoga maritima]	69	49
197	4	3571	4602	gi|1783251	homologous to cytochrome d ubiquinol oxidase subunit II; hypothetical [Bacillus subtilis]	69	46
197	6	6283	7701	gi|1783253	homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis]	69	49
222	1	201	10	gi|149901	gene codes for a 19 kDa protein [Mycobacterium avium] sp|P46733|19KD_MYCAV 19 KD LIPOPROTEIN ANTIGEN PRECURSOR.	69	50
223	28	23857	24567	gnl|PID|e269548	Unknown [Bacillus subtilis]	69	53
228	3	2031	1285	gi|1742730	Protein AraJ precursor. [Escherichia coli]	69	45
229	8	7390	6698	gi|1162980	ribulose-5-phosphate 3-epimerase [Spinacia oleracea]	69	52
238	27	25243	25695	gi|305005	ORF_f104 [Escherichia coli]	69	53
253	3	1067	921	gi|1591278	aspartokinase I [Methanococcus jannaschii]	69	39
260	4	2110	3105	gi|580841	F1 [Bacillus subtilis]	69	45
268	3	2287	1910	gi|460026	repressor protein [Streptococcus pneumoniae]	69	48
269	7	4532	4083	gi|1303792	YqeK [Bacillus subtilis]	69	50

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
271	15	11040	12236	gi|1303805	YqeR [Bacillus subtilis]	69	48
271	16	12444	12809	gi|435490	orf1 gene product [Lactococcus lactis]	69	46
281	3	1277	2068	gi|1303968	YqjQ [Bacillus subtilis]	69	50
281	6	5004	5534	gi|1773151	adenine phosphoribosyltransferase [Escherichia coli]	69	54
292	24	19939	18398	gi|1652664	glutamine-binding periplasmic protein [Synechocystis sp.]	69	45
323	3	2708	4243	gi|179401	beta-D-galactosidase precursor (EC 3.2.1.23) [Homo sapiens] gi|179423 beta-galactosidase precursor (EC 3.2.1.23) [Homo sapiens] pir|A32688|A32611 beta-galactosidase (EC 3.2.1.23) precursor - uman	69	56
330	2	1388	2353	gi|1303783	YqeC [Bacillus subtilis]	69	48
332	1	2	223	gi|1653594	hemolysin [Synechocystis sp.]	69	50
338	9	7035	7607	gi|467442	stage V sporulation [Bacillus subtilis]	69	55
341	1	1	408	gi|1477741	histidine periplasmic binding protein P29 [Campylobacter jejuni]	69	50
368	2	972	598	gi|516826	rat GCP360 [Rattus rattus]	69	33
375	4	3405	2599	gi|1215693	putative orf; GT9_orf434 [Mycoplasma pneumoniae]	69	38
386	1	2	166	gi|1549376	putative protein [Synechococcus PCC7942]	69	42
396	4	1248	1715	gi|410132	ORFX8 [Bacillus subtilis]	69	50
398	4	2763	2927	gi|466475	putative phospho-beta-glucosidase [Bacillus stearothermophilus] pir|D49898|D49898 cellobiose phosphotransferase system celC - acillus stearothermophilus	69	55
421	5	2950	3471	gi|1574625	H. influenzae predicted coding region HI1074 [Haemophilus influenzae]	69	45
423	4	2408	2893	gnl|PID|e163522	rnhB [Haemophilus influenzae]	69	55
436	3	1763	1521	gi|155032	ORF B [Plasmid pEa34]	69	37

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
452	1	3	341	gi|1591139	M. jannaschii predicted coding region MJ0435 [Methanococcus jannaschii]	69	52
470	3	1816	2181	gi|437389	transposase [Lactococcus lactis]	69	56
471	2	2003	813	gi|854233	cymF gene product [Klebsiella oxytoca]	69	49
478	1	822	4	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] gnl|PID|e255102 deoxyribodipyrimidine photolyase [Bacillus ubtilis]	69	63
490	4	1447	1289	gi|699379	glvr-1 protein [Mycobacterium leprae]	69	41
518	2	213	605	pir|S00076|R5BS12	ribosomal protein L12 - Bacillus stearothermophilus	69	59
536	4	1471	1653	gi|1146240	ketopantoate hydroxymethyltransferase [Bacillus subtilis]	69	53
539	5	3796	5091	gi|973231	gamma-glutamyl phosphate reductase [Lycopersicon esculentum]	69	54
566	1	1	231	gi|45741	ORFE [Enterococcus faecalis]	69	50
579	5	2729	3595	gi|145887	malonyl coenzyme A-acyl carrier protein transacylase [Escherichia oli]	69	49
583	2	373	912	gi|1064791	function umknown [Bacillus subtilis]	69	55
605	1	254	3	pir|S39743|S39743	hypothetical protein - Bacillus subtilis	69	37
630	2	1659	1231	gi|153672	lactose repressor [Streptococcus mutans]	69	47
634	1	36	731	gi|1022725	unknown [Staphylococcus haemolyticus]	69	53
662	1	486	73	gi|467431	high level kasgamycin resistance [Bacillus subtilis] sp|P37468|KSGA_BACSU DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) 16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESISTANCE PROTEIN SGA) (K	69	55
689	1	340	26	gi|1017817	membrane spanning protein [Streptomyces coelicolor]	69	41
756	2	300	500	gi|520596	Mre2 protein [Saccharomyces cerevisiae]	69	46

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
792	2	855	460	gi|1303823	YqfG [Bacillus subtilis]	69	55
916	1	4	789	gnl|PID|e253114	ornithine carbamoyltransferase [Pyrococcus furiosus]	69	57
7	3	2609	3748	gi|1303836	YqfO [Bacillus subtilis]	68	50
16	5	4165	4689	gi|142450	ahrC protein [Bacillus subtilis]	68	46
17	16	12826	13071	gi|222681	RNA polymerase [Tomato spotted wilt virus]	68	50
17	32	31402	31572	gi|1303984	YqkG [Bacillus subtilis]	68	44
17	33	31509	32009	gi|1303984	YqkG [Bacillus subtilis]	68	50
29	1	19	282	gi|1234787	up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region [Xenopus laevis]	68	37
29	3	1087	1950	gi|407878	leucine rich protein [Streptococcus equisimilis]	68	45
45	1	204	959	gi|1039479	ORFU [Lactococcus lactis]	68	50
47	7	8108	7527	gi|142853	homologous to unidentified E. coli protein [Bacillus subtilis] gi|143161 maf [Bacillus subtilis]	68	46
52	6	4304	5050	gnl|PID|e124050	alpha-acetolactate decarboxylase [Lactococcus lactis]	68	53
58	5	5961	4807	gi|466365	potential NAD-reducing hydrogenase subunit [Desulfovibrio ructosovorans]	68	49
68	8	4036	4743	gi|1673727	(AE000009) Mycoplasma pneumoniae, glutamine transport ATP-binding protein; similar to Swiss-Prot Accession Number P10346, from E. coli [Mycoplasma pneumoniae]	68	44
72	5	4441	3434	gi|1395209	ribonucleotide reductase R2-2 small subunit [Mycobacterium tuberculosis]	68	52
80	1	836	3	gi|474176	regulator protein [Staphylococcus xylosus]	68	48
81	2	793	1359	gi|1064809	homologous to sp:HTRA_ECOLI [Bacillus	68	48

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					subtilis]		
85	9	6911	6711	gi|144893	butyrate kinase [Clostridium acetobutylicum]	68	55
89	8	7184	5970	gi|1469784	putative cell division protein ftsW [Enterococcus hirae]	68	44
91	3	828	1076	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis]	68	53
103	1	1019	3	gi|143365	phosphoribosyl aminoimidazole carboxylase II (PUR-K; ttg start odon) [Bacillus subtilis]	68	50
106	2	2441	1509	gi|146860	delta-2-isopentenyl pyrophosphate transferase [Escherichia coli] gi|537012 tRNA delta-2-isopentenylpyrophosphate (IPP) transferase Escherichia coli]	68	47
112	1	558	100	gnl|PID|e242290	carbamate kinase [Clostridium perfringens]	68	50
116	3	2383	1496	gi|755601	unknown [Bacillus subtilis]	68	42
119	3	2136	1201	gi|1171125	thioredoxin reductase [Clostridium litorale]	68	49
121	4	3697	4650	gi|790945	aryl-alcohol dehydrogenase [Bacillus subtilis]	68	48
123	26	24262	24801	gi|537235	Kenn Rudd identifies as gpmB [Escherichia coli]	68	51
123	27	24887	25888	gi|143150	levR [Bacillus subtilis]	68	51
126	4	2773	1844	gi|551854	ORF2 [Erwinia herbicola]	68	54
131	1	150	1058	gi|1387979	44% identity over 302 residues with hypothetical protein from Synechocystis sp, accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtil	68	44
134	3	2154	1804	sp|P39213|YI91_SHI	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7	68	43

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
				DY	KD PROTEIN.		
138	19	12285	12656	gi|1438847	homologue of hypothetical 17.6 kDa protein in rplI-cpdB intergenic region of E. coli [Bacillus subtilis]	68	43
151	2	2784	1654	gi|143365	phosphoribosyl aminoimidazole carboxylase II (PUR-K; ttg start odon) [Bacillus subtilis]	68	45
164	23	24352	24119	gi|1573564	hypothetical [Haemophilus influenzae]	68	40
166	2	970	1260	gi|151968	nifS [Rhodobacter sphaeroides]	68	41
172	2	1320	2015	gi|1208965	hypothetical 23.3 kd protein [Escherichia coli]	68	46
175	1	900	451	gi|468207	Submitter comments: A Mg2+ transporting P-type ATPase highly omologous with mgtB ATPase at 80 min on Salmonella chromosome. ediates the influx of Mg2+ only. . Transcription regulated by xtracellular Mg2+ [Salmonella typhimurium]	68	47
180	14	12551	14956	gi|565641	FdrA protein [Escherichia coli]	68	49
186	1	3	686	gi|405804	transposase [Streptococcus thermophilus]	68	51
200	1	239	3	gi|468016	immunoglobulin heavy chain binding protein [Giardia intestinalis]	68	42
201	4	4468	3686	gi|304013	abcA [Aeromonas salmonicida]	68	50
204	10	6833	6468	gi|488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	68	51
214	3	3360	2491	gi|928834	integrase [Lactococcus lactis phage BK5-T]	68	50
229	9	8277	7375	gi|1574569	hypothetical [Haemophilus influenzae]	68	41
229	14	14288	13740	gnl|PID|e290287	polypeptide deformylase [Bacillus subtilis]	68	50
230	5	4593	3532	gi|143002	proton glutamate symport protein [Bacillus caldotenax] pir|S26246|S26246 glutamate/aspartate transport protein - Bacillus aldotenax	68	29

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
244	1	1	891	gi|537080	ribonucleoside triphosphate reductase [Escherichia coli] pir|A47331|A47331 oxygen-sensitive ribonucleoside-triphosphate eductase (EC 1.17.4.-) - Escherichia coli	68	54
244	5	4249	3551	gi|1773172	hypothetical protein [Escherichia coli]	68	46
244	7	5670	5212	gi|467423	unknown [Bacillus subtilis]	68	43
264	9	3925	3734	gi|914991	Similar to hemoglobinase [Saccharomyces cerevisiae] pir|S59796|S59796 hypothetical protein D9798.2 - yeast Saccharomyces cerevisiae)	68	44
271	7	3484	4686	gi|1469784	putative cell division protein ftsW [Enterococcus hirae]	68	50
271	11	6817	6548	gi|413948	ipa-24d gene product [Bacillus subtilis]	68	50
288	3	1638	1333	gi|562039	NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii] pir|S53835|S53835 NADH dehydrogenase chain 2 - Acanthamoeba astellanii mitochondrion (SGC6)	68	50
295	6	3537	4472	gi|555668	glycosylasparaginase precursor [Flavobacterium meningosepticum]	68	41
296	2	3143	1950	gi|1742630	Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli]	68	34
301	3	3271	1760	gi|413960	ipa-36d galT gene product [Bacillus subtilis]	68	53
315	3	2230	905	gi|1653498	ABC transporter [Synechocystis sp.]	68	47
318	2	1285	854	gi|43940	EIII-F Sor PTS [Klebsiella pneumoniae]	68	39
320	2	1178	621	gi|664842	sister of P-glycoprotein [Sus scrofa domestica]	68	46
331	2	342	566	pir|B48396|B48396	ribosomal protein L33 - Bacillus stearothermophilus	68	59

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
336	1	1	663	gi|1006591	cation-transporting ATPase PacL [Synechocystis sp.]	68	44
338	6	4004	5035	gi|155276	aldehyde dehydrogenase [Vibrio cholerae]	68	51
338	12	10404	11165	gi|467444	transcription-repair coupling factor [Bacillus subtilis] sp|P37474|MFD_BACSU TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF).	68	46
341	3	743	1222	gi|1183886	integral membrane protein [Bacillus subtilis]	68	45
351	6	2992	2561	gi|580881	ipa-73d gene product [Bacillus subtilis]	68	53
363	8	12517	9950	gi|1652980	H(+)-transporting ATPase [Synechocystis sp.]	68	46
368	3	1269	1736	gnl|PID|e209005	homologous to ORF2 in nrdEF operons of E.coli and S.typhimurium [Lactococcus lactis]	68	37
386	11	6564	6115	gi|765072	ORF3 [Staphylococcus aureus]	68	46
395	3	935	729	gi|15521	ORF 3 (AA 1-90) [Bacteriophage phi-105]	68	34
399	8	6073	6519	gi|153584	biotin carboxyl carrier protein [Streptococcus mutans] sp|P29337|BCCP_STRMU BIOTIN CARBOXYL CARRIER PROTEIN (BCCP).	68	53
408	3	2289	1336	gi|41572	GlnP (AA 1-219) [Escherichia coli]	68	40
420	1	559	2	gi|1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	68	51
423	2	254	1294	gi|1773109	similar to S. typhimurium apbA [Escherichia coli]	68	47
423	3	1465	2421	gi|1653032	hypothetical protein [Synechocystis sp.]	68	40
428	1	859	2	gi|1652454	hypothetical protein [Synechocystis sp.]	68	48
432	7	4626	3901	gi|1573285	hypothetical [Haemophilus influenzae]	68	55
434	1	90	1889	gi|1542975	AbcB [Thermoanaerobacterium thermosulfurigenes]	68	50
441	5	4674	5156	gi|467437	unknown [Bacillus subtilis]	68	48

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
455	4	3835	4080	gi|19815	luminal binding protein (BiP) [Nicotiana tabacum]	68	40
530	2	394	546	gi|763326	unknown [Saccharomyces cerevisiae]	68	42
531	2	810	622	gi|1146183	putative [Bacillus subtilis]	68	51
537	3	1353	1192	gi|929968	ORFA; similar to B. anthracis WeyAR element ORFA; putative ransposase [Bacillus anthracis]	68	56
539	3	2725	2231	gi|1353537	dUTPase [Bacteriophage r1t]	68	53
569	1	3	446	gi|146544	18 kD protein [Escherichia coli]	68	47
591	2	656	174	gi|1039479	ORFU [Lactococcus lactis]	68	42
652	2	739	1032	gi|1303715	YrkP [Bacillus subtilis]	68	50
671	2	436	1617	gi|413959	ipa-35d galK gene product [Bacillus subtilis]	68	50
684	1	466	2	gnl|PID|e248400	orfRM1 gene product [Bacillus subtilis]	68	40
693	1	2	787	gi|405804	transposase [Streptococcus thermophilus]	68	46
700	2	772	596	gi|153801	enzyme scr-II [Streptococcus mutans]	68	50
735	1	118	609	gi|969027	gamma-aminobutyrate permease [Bacillus subtilis] sp|P46349|GABP_BACSU GABA PERMEASE (4-AMINO BUTYRATE TRANSPORT ARRIER) (GAMA-AMINOBUTYRATE PERMEASE).	68	40
750	1	2	529	gi|893358	PgsA [Bacillus subtilis]	68	54
762	2	1588	950	gi|1146240	ketopantoate hydroxymethyltransferase [Bacillus subtilis]	68	49
790	1	407	3	gi|142224	attachment protein ChvA (ttg strart codon) [Agrobacterium umefaciens]	68	55
882	1	3	278	gi|57572	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) attus rattus]	68	48
950	1	140	568	gi|882736	ORF_f278 [Escherichia coli]	68	53
969	2	554	339	gi|1118031	similar to neural cell adhesion molecules and neuroglians in their IG-like C2-type domains [Caenorhabditis elegans]	68	47

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
970	1	297	73	gi|474404	cyclophilin [Tolypocladium inflatum]	68	40
1	1	1103	3	gi|48790	ORF 3 [Pseudomonas putida]	67	50
29	10	7156	6614	sp|P36672|PTTB_ECOLI	PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69)' (EII-TRE).	67	52
48	8	8035	9141	gi|975627	N-acylamino acid racemase [Amycolatopsis sp.]	67	48
55	12	6621	7439	gi|391610	farnesyl diphosphate synthase [Bacillus stearothermophilus] pir|JX0257|JX0257 geranyltranstransferase (EC 2.5.1.10) - Bacillus tearothermophilus	67	47
57	13	13972	16401	gnl|PID|e255138	phenylalanyl-tRNA synthetase beta subunit [Bacillus subtilis]	67	47
63	4	1917	2729	gi|1321629	MIP related protein of E. coli [Escherichia coli]	67	47
68	12	8600	8923	gi|793910	surface antigen [Homo sapiens]	67	43
72	7	7138	6740	gnl|PID|e209005	homologous to ORF2 in nrdEF operons of E.coli and S.typhimurium [Lactococcus lactis]	67	39
72	10	8309	9433	gi|1199515	ferrous iron transport protein B [Escherichia coli]	67	41
85	5	5315	4296	gi|142611	branched chain alpha-keto acid dehydrogenase E1-alpha [Bacillus ubtilis]	67	52
101	5	4149	3100	gi|1109686	ProX [Bacillus subtilis]	67	48
110	4	2335	1292	gi|1066343	mu-crystallin [Homo sapiens]	67	48
114	12	12936	13520	gi|146218	serine hydroxymethyltransferase [Escherichia coli]	67	50
115	5	3137	2010	gi|1256150	YbaR [Bacillus subtilis]	67	47
115	6	3199	2792	gi|1652593	hypothetical protein [Synechocystis sp.]	67	45
123	25	22739	24208	gi|148711	6-aminohexanoate-cyclic-dimer hydrolase [Flavobacterium sp.] gi|488343 6-	67	50

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					aminohexanoate-cyclic-dimer hydrolase [Flavobacterium p.]		
124	6	5139	4267	gi|1016770	prolipoprotein diacylglyceryl transferase [Staphylococcus aureus]	67	50
125	2	1306	221	gi|853743	L-alanoyl-D-glutamate peptidase [Bacteriophage A118]	67	50
128	36	29462	28737	gi|142940	ftsA [Bacillus subtilis]	67	46
138	27	17602	18183	gi|1256639	putative [Bacillus subtilis]	67	50
138	31	21578	20097	gi|143245	Na+/H+ antiporter [Bacillus firmus]	67	42
138	33	25165	23249	gi|1498811	M. jannaschii predicted coding region MJ0050 [Methanococcus jannaschii]	67	45
138	36	28690	27362	gnl|PID|e269549	Unknown [Bacillus subtilis]	67	47
144	4	3271	3717	gi|1753229	PKCI [Borrelia burgdorferi]	67	52
145	3	1435	2511	gi|1573615	ATP-binding protein (abc) [Haemophilus influenzae]	67	47
146	5	4657	2804	gi|1045034	beta-galactosidase [Xanthomonas campestris pv. manihotis]	67	51
149	3	1978	1367	gi|806536	membrane protein [Bacillus acidopullulyticus]	67	51
156	1	3	365	gnl|PID|e265539	ClpB-homologue [Thermus aquaticus thermophilus]	67	42
158	15	14863	13766	gi|1573487	rbs repressor (rbsR) [Haemophilus influenzae]	67	40
158	17	16483	15959	gi|677850	hypothetical protein [Staphylococcus aureus]	67	51
159	7	6872	6006	gi|1303949	YqiX [Bacillus subtilis]	67	41
159	9	8103	7498	gi|1303950	YqiY [Bacillus subtilis]	67	41
165	11	9846	9004	gi|606079	ORF_o267 [Escherichia coli]	67	36
169	2	2151	3047	gi|42371	pyruvate formate-lyase activating enzyme (AA 1-246) [Escherichia li]	67	44
179	13	13648	14451	gnl|PID|e257631	methyltransferase [Lactococcus lactis]	67	45

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
180	28	28656	29801	gi|666005	hypothetical protein [Bacillus subtilis]	67	48
194	6	2774	4231	gi|143245	Na+/H+ antiporter [Bacillus firmus]	67	41
194	10	6472	8259	gi|622991	mannitol transport protein [Bacillus stearothermophilus] sp|P50852|PTMB_BACST PTS SYSTEM, MANNITOL-SPECIFIC IIBC COMPONENT EIIBC-MTL) (MANNITOL- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE NZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-MTL).	67	50
204	5	1924	3006	gi|1235684	mevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae]	67	50
214	1	42	1196	gi|606013	CG Site No. 829 [Escherichia coli]	67	36
219	2	524	850	gnl|PID|e257628	ORF [Lactococcus lactis]	67	42
223	15	13640	14407	gi|496520	orf iota [Streptococcus pyogenes]	67	54
227	3	1011	1892	gi|1070013	protein-dependent [Bacillus subtilis]	67	37
233	12	9340	8339	gi|507880	xanthine dehydrogenase [Gallus gallus]	67	50
238	10	7951	9183	gi|1653948	hypothetical protein [Synechocystis sp.]	67	45
246	3	783	1430	gnl|PID|e233869	hypothetical protein [Bacillus subtilis]	67	47
256	2	570	1601	gi|709992	hypothetical protein [Bacillus subtilis]	67	36
266	2	1266	835	gi|963038	ArpU [Enterococcus hirae]	67	42
285	1	3	809	gi|40014	pot. ORF 446 (aa 1-446) [Bacillus subtilis]	67	53
288	10	6838	5801	gi|1651806	hypothetical protein [Synechocystis sp.]	67	45
301	10	8822	8562	gi|1303864	YqgQ [Bacillus subtilis]	67	43
312	5	2377	2595	gi|709991	hypothetical protein [Bacillus subtilis]	67	52
353	1	3	1472	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	67	48
359	2	984	439	gi|1773190	similar to E. coli yhaE [Escherichia coli]	67	45
359	3	2244	982	gi|1001478	hypothetical protein [Synechocystis sp.]	67	30
364	8	8469	7816	gi|496943	ORF [Saccharomyces cerevisiae]	67	50

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
386	12	6625	7833	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	67	36
394	2	497	2635	gnl|PID|e255093	hypothetical protein [Bacillus subtilis]	67	45
399	6	5410	3971	gi|665994	hypothetical protein [Bacillus subtilis]	67	45
414	1	1	1227	gi|1621027	high affinity potassium transporter [Debaryomyces occidentalis]	67	40
453	2	618	391	gi|537189	ORF_f132 [Escherichia coli]	67	45
458	1	825	226	gnl|PID|e189917	ORF 28.5 [Escherichia coli]	67	45
460	2	644	1387	gi|1502421	3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis]	67	48
460	4	2622	3131	gi|1399830	biotin carboxyl carrier protein [Synechococcus PCC7942]	67	53
474	1	1456	77	gi|495277	histidine kinase [Streptococcus pneumoniae]	67	54
488	6	3892	3032	gi|437389	transposase [Lactococcus lactis]	67	47
490	1	460	2	gi|1742830	ORF_ID:o326#2; similar to [SwissProt Accession Number P37794] [Escherichia coli]	67	43
582	1	2	787	gi|1408485	yxdM gene product [Bacillus subtilis]	67	38
629	2	1280	915	gi|1006620	ABC transporter [Synechocystis sp.]	67	50
633	2	941	390	gnl|PID|e221400	tex gene product [Bordetella pertussis]	67	54
655	1	47	313	gi|147403	mannose permease subunit II-P-Man [Escherichia coli]	67	48
671	3	1630	2415	sp|P13226|GALE_STRLI	UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE).	67	52
682	2	1428	595	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	67	42
704	3	977	411	gi|467428	unknown [Bacillus subtilis]	67	45
711	1	590	168	gi|471236	orf3 [Haemophilus influenzae]	67	37
784	1	253	2	gnl|PID|e236287	site-specific DNA-methyltransferase [Bacillus stearothermophilus]	67	44

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
907	1	209	3	gi|5119	topoisomerase I [Schizosaccharomyces pombe]	67	42
908	1	275	96	gi|1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	67	46
960	1	499	98	gi|405804	transposase [Streptococcus thermophilus]	67	50
963	1	259	2	pir|S34632|S34632	dnaJ protein homolog - human	67	54
964	1	164	628	bbs|173803	CD4+ T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167, Peptide Partial, 268 aa] [Listeria monocytogenes]	67	49
5	4	1438	2403	gi|1303810	YqeT [Bacillus subtilis]	66	50
7	1	24	1727	gi|145220	alanyl-tRNA synthetase [Escherichia coli]	66	50
7	2	1858	2646	gi|687599	orfA1; transposon insertion into orfA1 impairs growth and virulence f L. monocytogenes [Listeria monocytogenes]	66	58
8	1	3	707	gi|1303830	YqfL [Bacillus subtilis]	66	45
9	1	182	1051	gi|467399	IMP dehydrogenase [Bacillus subtilis]	66	51
17	11	8383	8598	gi|457336	Pv200 [Plasmodium vivax]	66	42
18	14	5903	6136	gi|294706	trfA [Plasmid RK2]	66	50
23	12	5951	6895	gi|1652472	ethylene response sensor protein [Synechocystis sp.]	66	51
23	17	11198	11881	gi|466517	pduB [Salmonella typhimurium]	66	44
23	19	12395	13501	gi|145206	alcohol dehydrogenase (adhE) [Escherichia coli]	66	47
34	5	5987	6232	gi|397360	yNucR endo-exonuclease [Saccharomyces cerevisiae]	66	46
43	2	782	1018	gi|513417	non-structural polyprotein of pSP6-SFV4 [unidentified]	66	46
43	5	3757	2324	gnl|PID|e154145	penicillin binding protein 4 [Staphylococcus aureus]	66	44
56	4	2351	1662	gi|49272	Asparaginase [Bacillus licheniformis]	66	44
57	2	950	1735	gi|1657505	hypothetical protein [Escherichia coli]	66	46

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
57	4	3117	3932	gi|1657507	hypothetical protein [Escherichia coli]	66	41
57	8	12269	12646	gi|1622733	orf108; unknown function [Butyrivibrio fibrisolvens]	66	44
62	2	547	1302	gi|413967	ipa-43d gene product [Bacillus subtilis]	66	50
62	5	2633	1905	gi|475110	fructokinase [Pediococcus pentosaceus]	66	51
74	7	4661	4086	gi|467484	unknown [Bacillus subtilis]	66	47
81	18	13878	13717	gi|146724	enzyme III-Man function protein (manX (ptsL)) [Escherichia coli] gi|41976 manX gene product (AA 1-315) [Escherichia coli]	66	35
94	17	20780	21253	gi|142955	glucose dehydrogenase (EC 1.1.1.47) [Bacillus subtilis] pir|S36090|S36090 glucose 1-dehydrogenase (EC 1.1.1.47) - Bacillus ubtilis	66	47
98	15	15165	14338	gi|147327	transport protein [Escherichia coli]	66	34
105	3	1726	3183	gnl|PID|e205173	orf1 gene product [Lactobacillus helveticus]	66	45
110	17	15811	14804	gi|887824	ORF_o310 [Escherichia coli]	66	52
112	2	712	443	gnl|PID|e242290	carbamate kinase [Clostridium perfringens]	66	51
123	1	1	540	gi|1573538	H. influenzae predicted coding region HI0552 [Haemophilus influenzae]	66	39
123	33	30312	31460	gi|1498930	M. jannaschii predicted coding region MJ0158 [Methanococcus jannaschii]	66	48
125	8	4914	4474	gi|1736749	Exopolysaccharide production protein PSS. [Escherichia coli]	66	54
128	25	18201	18878	gnl|PID|e255543	putative iron dependant repressor [Staphylococcus epidermidis]	66	48
131	3	2311	3213	gi|38969	lacF gene product [Agrobacterium radiobacter]	66	37
131	5	3588	3394	gi|1303823	YqfG [Bacillus subtilis]	66	29
135	1	1214	45	gi|1498930	M. jannaschii predicted coding region MJ0158 [Methanococcus jannaschii]	66	48
135	10	7764	7405	gi|530825	OVT1 [Onchocerca volvulus]	66	47

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
144	13	12859	10739	pir|A40614|A40614	penicillin-binding protein pbpF - Bacillus subtilis	66	47
145	5	3224	4063	gi|349531	lipoprotein [Pasteurella haemolytica]	66	45
146	2	1497	619	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	66	38
149	2	1097	1282	gi|1762962	FemA [Staphylococcus simulans]	66	38
150	3	1443	2417	gnl|PID|e185374	ceuE gene product [Campylobacter coli]	66	46
150	8	6487	6903	gi|1377842	unknown [Bacillus subtilis]	66	43
164	20	21846	22646	gi|1279769	FdhC [Methanobacterium thermoformicicum]	66	57
164	25	24555	25688	pir|A43577|A43577	regulatory protein pfoR - Clostridium perfringens	66	47
178	1	383	3	gi|763052	integrase [Bacteriophage T270]	66	47
195	19	8698	8516	bbs|169008	homeobox gene [Drosophila sp.]	66	55
207	1	166	1554	gi|619724	MgtE [Bacillus firmus]	66	39
207	3	2312	2010	gi|1204258	soluble protein [Escherichia coli]	66	44
211	3	1523	1729	gi|289932	MHC class II beta chain [Cyphotilapia frontosa]	66	66
213	3	1811	2308	gi|153045	prolipoprotein signal peptidase [Staphylococcus aureus] pir|S20433|S20433 lsp protein - Staphylococcus aureus sp|P31024|LSPA_STAAU LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.36) PROLIPOPROTEIN SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II).	66	40
221	7	2524	3468	gi|1353527	ORF10 [Bacteriophage r1t]	66	44
222	13	8272	8988	gi|466719	No definition line found [Escherichia coli]	66	48
223	18	15210	15971	gi|496520	orf iota [Streptococcus pyogenes]	66	57
232	5	3494	2715	gi|142706	comG1 gene product [Bacillus subtilis]	66	41
235	3	1774	734	gi|580897	OppB gene product [Bacillus subtilis]	66	47
244	2	906	1520	gi|15354	ORF 55.9 [Bacteriophage T4]	66	46

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
259	3	2355	1867	gi|56312	Gephyrin [Rattus norvegicus]	66	55
271	1	1	675	gi|1574748	tRNA pseudouridine 55 synthase (truB) [Haemophilus influenzae]	66	53
277	1	1	927	gi|1303799	YqeN [Bacillus subtilis]	66	45
291	5	4587	3547	gnl|PID|e257609	sugar-binding transport protein [Anaerocellum thermophilum]	66	46
292	25	20451	19912	gi|1649035	high-affinity periplasmic glutamine binding protein [Salmonella typhimurium]	66	50
300	1	2302	77	gi|289262	comE ORF3 [Bacillus subtilis]	66	46
301	4	4290	3265	sp|P13226|GALE_STRLI	UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE).	66	51
301	5	4516	4689	gnl|PID|e212164	PSII, protein N [Odontella sinensis]	66	58
314	1	360	4	gi|467452	unknown [Bacillus subtilis]	66	43
315	4	2559	2209	gi|1653498	ABC transporter [Synechocystis sp.]	66	44
320	3	2406	1081	gnl|PID|e250352	unknown [Mycobacterium tuberculosis]	66	35
332	2	157	921	gi|1303875	YqhB [Bacillus subtilis]	66	44
334	2	1001	3076	gi|1651660	DNA ligase [Synechocystis sp.]	66	48
338	1	2	616	gi|845686	ORF-27 [Staphylococcus aureus]	66	54
338	7	5011	5496	gi|912476	No definition line found [Escherichia coli]	66	48
341	5	1935	3107	gi|142538	aspartate aminotransferase [Bacillus sp.]	66	44
343	3	2548	2045	gnl|PID|e289147	similar to single strand binding protein [Bacillus subtilis]	66	44
345	20	22093	22461	gi|1657795	dihydroneopterin aldolase [Methylobacterium extorquens]	66	45
353	3	2621	2379	gnl|PID|e257628	ORF [Lactococcus lactis]	66	52
365	4	5117	4779	gi|1742868	Mutator MutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (8-oxo-dgtpase) (EC 3.6.1.-) (DGTP pyrophosphohydrolase). [Escherichia coli]	66	54
376	1	3	1076	gi|1778517	glycerol dehydrogenase homolog	66	45

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Escherichia coli]		
394	7	5980	5648	gi|486358	ORF YKL202w [Saccharomyces cerevisiae]	66	38
421	4	1469	2539	gi|606375	ORF_f345 [Escherichia coli]	66	48
475	6	3978	3763	gi|532547	ORF14 [Enterococcus faecalis]	66	48
491	8	7710	7081	gi|1000453	TreR [Bacillus subtilis]	66	49
526	1	392	3	gi|1750125	xylulose kinase [Bacillus subtilis]	66	49
552	6	6147	5917	gi|1432152	PTS antiterminator [Klebsiella oxytoca]	66	37
571	2	560	1153	gi|1773132	multidrug resistance-like ATP-binding protein Mdl [Escherichia coli]	66	38
575	3	1075	539	gi|1651722	guanylate kinase [Synechocystis sp.]	66	48
608	2	631	113	gi|1213334	OrfX; hypothetical 22.5 KD protein downstream of type IV prepilin leader peptidase gene; Method: conceptual translation supplied by author [Vibrio vulnificus]	66	41
640	1	877	2	sp|P50487|YCPX_CLOPE	HYPOTHETICAL PROTEIN IN CPE 5'REGION (FRAGMENT).	66	36
734	1	2	343	gi|1653602	hypothetical protein [Synechocystis sp.]	66	43
802	1	2	292	gnl|PID|e280516	voltage-gated sodium channel [Mus musculus]	66	58
812	2	343	531	gi|511075	ORF2 [Streptococcus agalactiae]	66	51
823	1	1	393	gi|1303843	YqfV [Bacillus subtilis]	66	42
891	1	82	402	gi|567769	ORF5; predicted protein shows similarity to ATP-binding transport roteins AmiE and AmiF of Streptococcus pneumoniae; disruptuion of RF5 leads to aminopterin resistance [Streptococcus parasanguis]	66	52
5	6	2630	3154	gi|1303811	YqeU [Bacillus subtilis]	65	50
6	1	2	628	gi|1742303	Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (fragment). [Escherichia coli]	65	43
18	6	3360	2518	gi|601880	rep protein [Bacillus borstelensis]	65	40

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
21	11	7933	7706	gi|1500521	M. jannaschii predicted coding region MJ1623 [Methanococcus jannaschii]	65	32
23	20	13459	13881	gi|488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	65	43
23	25	15987	16178	gnl|PID|e248966	F32D8.5 [Caenorhabditis elegans]	65	50
27	2	526	302	gi|1001644	regulatory components of sensory transduction system [Synechocystis sp.]	65	44
29	9	6770	5727	sp|P36672|PTTB_ECOLI	PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-TRE).	65	45
31	5	4611	5207	gi|171625	guanylate kinase [Saccharomyces cerevisiae]	65	39
32	7	4085	3915	gi|150158	29 kD protein [Mycoplasma genitalium]	65	51
33	8	7396	7638	gi|1573421	protein translocation protein, low temperature (secG) [Haemophilus influenzae]	65	26
35	1	2	499	gi|1737500	transcription antiterminator [Bacillus stearothermophilus]	65	40
45	6	2537	3037	gi|511455	unknown [Coxiella burnetii]	65	37
46	3	1028	2254	gi|1001642	dGTP triphosphohydrolase [Synechocystis sp.]	65	43
47	12	14524	14264	gi|150209	ORF 1 [Mycoplasma mycoides]	65	34
50	3	2866	2051	gi|1303830	YqfL [Bacillus subtilis]	65	40
57	11	12955	13332	gnl|PID|e254999	phenylalany-tRNA synthetase beta subunit [Bacillus subtilis]	65	51
62	1	2	484	gi|1573470	H. influenzae predicted coding region HI0491 [Haemophilus influenzae]	65	57
68	1	49	282	gi|1573250	aspartate aminotransferase (aspC) [Haemophilus influenzae]	65	52
72	2	567	1325	gi|466645	alternate name yhiD [Escherichia coli]	65	40
81	5	3711	2938	gi|1732200	PTS permease for mannose subunit IIPMan	65	43

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Vibrio furnissii]		
83	18	12506	12745	pir|D64042|D64042	ribosomal-protein-alanine acetyltransferase (rimI) homolog - Haemophilus influenzae (strain Rd KW20)	65	50
100	38	28229	28032	gi|183075	glial fibrillary acidic protein [Homo sapiens]	65	43
105	1	912	106	pir|S15248|YQBZCD	fimC protein - Dichelobacter nodosus (serotype D)	65	46
106	5	6097	5102	gi|1143204	ORF2; Method: conceptual translation supplied by author [Shigella sonnei]	65	44
109	3	1165	899	gi|1573390	hypothetical [Haemophilus influenzae]	65	55
110	7	5579	4257	pir|B44514|B44514	hypothetical protein 1 (vnfA 5' region) - Azotobacter vinelandii	65	43
120	3	1249	1632	sp|P54746|YBGB_ECOLI	HYPOTHETICAL PROTEIN IN HRSA 3'REGION (FRAGMENT).	65	48
122	2	896	1654	gi|1335913	unknown [Erysipelothrix rhusiopathiae]	65	48
145	4	2509	3210	gi|1208965	hypothetical 23.3 kd protein [Escherichia coli]	65	40
149	7	4407	3502	gi|145173	35 kDa protein [Escherichia coli]	65	46
154	8	5738	4926	gi|405804	transposase [Streptococcus thermophilus]	65	47
155	1	306	512	gi|285627	E.coli SecE homologous protein [Bacillus subtilis] pir|S39858|S39858 secE protein homolog - Bacillus subtilis sp|Q06799|SECE_BACSU PREPROTEIN TRANSLOCASE SECE SUBUNIT.	65	48
158	1	150	1103	gi|289272	ferrichrome-binding protein [Bacillus subtilis]	65	40
158	16	14885	15946	gi|467172	add; L308_C2_206 [Mycobacterium leprae]	65	36
173	4	2103	2912	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	65	41
173	12	9749	9054	gi|1652864	hypothetical protein [Synechocystis sp.]	65	50
179	16	15674	17035	gi|1171125	thioredoxin reductase [Clostridium litorale]	65	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
180	26	26911	28266	sp|P13692|P54_ENTFC	P54 PROTEIN PRECURSOR.	65	39
193	6	2893	3795	gi|39787	adaA [Bacillus subtilis]	65	45
194	5	1843	2238	gi|47394	5-oxoprolyl-peptidase [Streptococcus pyogenes]	65	48
199	1	894	82	gi|1591118	nitrate transport ATP-binding protein [Methanococcus jannaschii]	65	46
200	24	13441	13136	gi|144926	toxin A [Clostridium difficile]	65	39
202	3	2925	1846	gi|413968	ipa-44d gene product [Bacillus subtilis]	65	46
203	1	797	3	gi|1377832	unknown [Bacillus subtilis]	65	45
204	3	1065	1472	gi|1008996	unknown [Schizosaccharomyces pombe]	65	51
205	4	1029	1685	gi|148989	truncated tetracycline resistance repressor (non-functional) Haemophilus parainfluenzae]	65	42
206	8	5037	4807	pir|D60110|D60110	repetitive protein antigen 3 - Trypanosoma cruzi (fragment)	65	41
217	1	411	4	gi|1146181	putative [Bacillus subtilis]	65	43
217	4	1092	3065	gi|984229	penicillin-binding protein 1a [Streptococcus pneumoniae]	65	48
223	27	23445	23879	gnl|PID|e269486	Unknown [Bacillus subtilis]	65	47
225	6	5138	3984	gi|39956	IIGlc [Bacillus subtilis]	65	47
229	5	5528	5130	gi|1303914	YghY [Bacillus subtilis]	65	33
229	10	10697	8517	gnl|PID|e266933	unknown [Mycobacterium tuberculosis]	65	46
233	3	2413	1526	gi|887825	ORF_f541 [Escherichia coli]	65	46
236	4	6975	4789	gi|405863	yohA [Escherichia coli]	65	43
237	4	1460	1816	gi|305080	myosin heavy chain [Entamoeba histolytica]	65	42
238	24	21690	23228	gi|305008	rhamnulokinase [Escherichia coli]	65	49
242	3	2192	3280	gnl|PID|e221269	tail protein [Bacteriophage CP-1]	65	37
244	6	5172	4228	gi|1653197	hypothetical protein [Synechocystis sp.]	65	51
259	5	3684	2779	gi|559900	F49E2.1 [Caenorhabditis elegans]	65	39
259	6	4243	3749	gi|1743887	molybdopterin cofactor biosynthesis enzyme	65	50

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Bradyrhizobium japonicum]		
260	1	140	478	gi|895748	putative cellobiose phosphotransferase enzyme II' [Bacillus ubtilis]	65	55
269	6	4113	3907	gi|1303792	YqeK [Bacillus subtilis]	65	39
271	12	7731	6772	gi|1657534	cyn operon transcriptional activator [Escherichia coli]	65	45
275	9	6413	5361	gi|1773132	multidrug resistance-like ATP-binding protein Mdl [Escherichia coli]	65	48
276	4	1813	1583	gi|1504014	similar to myosin heavy chain: Containing ATP/GTP-binding site motif A(P-loop) [Homo sapiens]	65	34
279	14	14254	10625	gi|1237015	ORF4 [Bacillus subtilis]	65	45
281	2	692	1279	gi|1303962	YqjK [Bacillus subtilis]	65	50
295	5	2279	3388	gi|436965	[malA] gene products [Bacillus stearothermophilus] pir|S43914|S43914 hypothetical protein 1 - Bacillus tearothermophilus	65	41
298	1	63	1142	gi|928834	integrase [Lactococcus lactis phage BK5-T]	65	44
301	8	7592	7176	gi|1303893	YqhL [Bacillus subtilis]	65	50
311	3	4658	5701	gnl|PID|e221269	tail protein [Bacteriophage CP-1]	65	40
326	1	2	247	gi|466520	pocR [Salmonella typhimurium]	65	38
329	1	789	523	gi|1303895	YqhN [Bacillus subtilis]	65	36
345	5	3363	3641	gi|895749	putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis]	65	51
369	3	1635	1207	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	65	45
373	2	815	1630	gi|1277032	unknown [Bacillus subtilis]	65	41
379	9	11301	8275	gi|887828	was o492p and o826p before splice [Escherichia coli]	65	49
386	13	7903	8145	gnl|PID|e217382	M7.9 [Caenorhabditis elegans]	65	39
395	4	1028	1231	gi|1592033	M. jannaschii predicted coding region	65	30

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					MJ1387 [Methanococcus jannaschii]		
396	3	1000	1272	gi|1045900	hypothetical protein (GB:L09228_17) [Mycoplasma genitalium]	65	44
422	3	2050	1262	gi|405907	yejD [Escherichia coli]	65	50
438	1	44	358	gi|530798	LysB [Bacteriophage phi-LC3]	65	39
460	1	119	646	gi|1502420	malonyl-CoA:Acyl carrier protein transacylase [Bacillus subtilis]	65	46
463	1	870	121	gi|1651917	tRNA(m1G37)methyltransferase [Synechocystis sp.]	65	47
468	1	2	823	gi|216457	ORF [Escherichia coli]	65	46
470	1	34	816	gi|530798	LysB [Bacteriophage phi-LC3]	65	47
476	1	21	830	gi|1006591	cation-transporting ATPase PacL [Synechocystis sp.]	65	46
510	7	4875	6092	gi|143150	levR [Bacillus subtilis]	65	46
565	2	686	339	gi|143833	PBSX repressor [Bacillus subtilis]	65	51
566	2	198	743	gi|496501	RepS [Streptococcus pyogenes]	65	34
604	5	1875	2078	gi|1590997	M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii]	65	49
608	1	194	3	gnl|PID|e290940	unknown [Mycobacterium tuberculosis]	65	35
648	1	60	953	gi|1591145	hypothetical protein (HI0902) [Methanococcus jannaschii]	65	31
657	4	2531	1620	gi|1500015	amidase [Methanococcus jannaschii]	65	46
691	1	2	718	gnl|PID|e248400	orfRM1 gene product [Bacillus subtilis]	65	48
704	2	474	175	gi|467428	unknown [Bacillus subtilis]	65	50
758	2	408	683	gi|451201	ORF1 [Bacillus subtilis]	65	44
778	1	833	3	gi|410137	ORFX13 [Bacillus subtilis]	65	40
793	1	1	564	gi|912436	oligo-1,6-glucosidase [Bacillus thermoglucosidasius] pir|A41707|A41707 oligo-1,6-glucosidase (EC 3.2.1.10) - Bacillus hermoglucosidasius	65	40
827	1	364	2	gi|852076	MrgA [Bacillus subtilis]	65	33

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
856	1	209	3	gi|1575605	4-methyl-5-nitrocatechol oxygenase [Burkholderia sp.]	65	45
890	1	966	745	pir|A44803|A44803	pG1 protein - human (fragment)	65	63
4	1	2	958	gnl|PID|e265530	yorfE [Streptococcus pneumoniae]	64	43
5	8	4212	5579	gi|407881	stringent response-like protein [Streptococcus equisimilis] pir|S39975|S39975 stringent response-like protein - Streptococcus quisimilis	64	47
8	4	4047	3304	gi|1573150	dihydrolipoamide acetyltransferase (acoC) [Haemophilus influenzae]	64	37
17	14	11709	10393	gi|155109	ORF 1B [Thermus aquaticus thermophilus]	64	37
19	12	6499	6801	gi|1303755	YqbO [Bacillus subtilis]	64	32
23	1	1	303	gi|1022963	dextransucrase [Leuconostoc mesenteroides]	64	50
28	4	7059	6505	gi|1568609	18kDA protein [Streptococcus pneumoniae]	64	45
31	3	1316	2986	gi|1100076	PTS-dependent enzyme II [Clostridium longisporum]	64	47
47	2	2665	3408	gi|1742154	Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli]	64	52
48	2	1699	1310	gi|142702	A competence protein 2 [Bacillus subtilis]	64	41
54	8	2750	2352	gi|951052	ORF9, putative [Streptococcus pneumoniae]	64	31
57	15	18035	17274	gi|1183886	integral membrane protein [Bacillus subtilis]	64	40
62	4	1968	1699	gi|475110	fructokinase [Pediococcus pentosaceus]	64	52
100	42	29329	29039	gi|951048	excisionase [Streptococcus pneumoniae]	64	37
102	4	3726	4805	gi|215331	morphogenesis protein [Bacteriophage phi-29]	64	43
106	3	3296	2439	gi|1303930	YqiK [Bacillus subtilis]	64	44
123	12	12960	11314	sp|P37047|YAEG_ECOLI	HYPOTHETICAL 44.3 KD PROTEIN IN HTRA-DAPD INTERGENIC REGION.	64	40
128	2	1285	1614	gi|143961	pyruvate phosphate dikinase [Clostridium symbiosum] pir|A36231|KIQAPO	64	52

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					pyruvate,orthophosphate dikinase (EC 2.7.9.1) - lostridium symbiosum		
128	8	6178	4757	gi|40665	beta-glucosidase [Clostridium thermocellum]	64	41
133	2	1748	2248	gi|1591027	ferripyochelin binding protein [Methanococcus jannaschii]	64	46
150	1	35	673	gnl|PID|e185372	ceuC gene product [Campylobacter coli]	64	38
158	6	6038	5040	gi|1045801	hypothetical protein (SP:P32720) [Mycoplasma genitalium]	64	35
164	7	3620	4903	gnl|PID|e283116	unknown similar to quinolon resistance protein NorA [Bacillus subtilis]	64	41
171	11	10107	10784	gi|1591668	phosphate transport system regulatory protein [Methanococcus jannaschii]	64	40
179	4	4826	6373	gi|149535	D-alanine activating enzyme [Lactobacillus casei]	64	51
181	4	2251	1364	gi|671632	unknown [Staphylococcus aureus]	64	38
190	11	11302	10355	gi|599850	orf1 gene product [Lactobacillus sake]	64	33
195	37	15344	16033	gi|1736499	Lysostaphin precursor (EC 3.5.1.-). [Escherichia coli]	64	49
199	4	4000	5631	gi|746574	similar to M. musculus transport system membrane protein, Nramp PIR:A40739) and S. cerevisiae SMF1 protein (PIR:A45154) Caenorhabditis elegans]	64	37
202	1	1	1560	gi|309662	pheromone binding protein [Plasmid pCF10]	64	45
204	7	3000	4115	gi|1591731	melvalonate kinase [Methanococcus jannaschii]	64	41
208	1	308	1090	gi|473821	'tetrahydrodipicolinate N-succinyltransferase' [Escherichia coli] gi|1552743 tetrahydrodipicolinate N-succinyltransferase Escherichia coli]	64	42
216	9	6501	6698	gi|47373	7 kDa protein [Streptococcus pneumoniae]	64	35
221	18	8268	8513	gi|1389837	complement regulatory protein [Trypanosoma	64	28

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					cruzi]		
231	4	2964	2632	gnl|PID|e279941	muconate cycloisomerase [Rhodococcus erythropolis]	64	37
234	2	751	302	gnl|PID|e194709	N-terminal part of a protein of unknown function [Chlamydia psittaci]	64	42
238	18	15580	16392	gi|537108	ORF_f254 [Escherichia coli]	64	44
245	1	14	868	gi|153247	endo-beta-N-acetylglucosaminidase H [Streptomyces plicatus] pir|A00903|RBSMHP mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) H precursor - treptomyces plicatus	64	51
272	2	584	1144	gi|580781	signal peptidase [Bacillus licheniformis]	64	47
281	5	2659	5019	gi|147550	recJ [Escherichia coli]	64	46
290	12	9496	10371	gi|45713	P.putida genes rpmH, rnpA, 9k, 60k, 50k, gidA, gidB, uncI and uncB seudomonas putida]	64	42
298	4	4029	3466	gi|147780	rts gene product [Escherichia coli]	64	43
301	20	16216	15977	gi|170482	prosystemin [Solanum lycopersicum]	64	57
301	21	17732	17391	gi|405804	transposase [Streptococcus thermophilus]	64	52
307	1	198	1964	gi|1255196	BSMA [Bacillus stearothermophilus]	64	48
320	5	3441	3070	gi|972900	ArtP [Haemophilus influenzae]	64	38
341	9	7690	6413	gi|1161380	IcaA [Staphylococcus epidermidis]	64	30
345	6	3589	4848	gi|902932	L-methionine gamma-lyase [Pseudomonas putida]	64	45
348	1	453	22	gi|1591957	M. jannaschii predicted coding region MJ1318 [Methanococcus jannaschii]	64	32
350	2	1372	1830	gnl|PID|e289141	similar to hydroxymyristoyl-(acyl carrier protein) dehydratase [Bacillus subtilis]	64	44
351	7	3291	2917	gi|49013	dTDP-dihydrostreptose synthase [Streptomyces griseus] ir|S18618|SYSMPG dTDP-dihydrostreptose synthase - Streptomyces iseus	64	46

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
352	2	780	1028	gi|173431	H+-ATPase [Schizosaccharomyces pombe]	64	38
386	10	5952	6161	gnl|PID|e243284	ORF YGL056c [Saccharomyces cerevisiae]	64	50
398	2	1233	1808	gi|147920	3-methyladenine-DNA glycosylase I (tag) [Escherichia coli]	64	47
399	12	8761	9159	gi|1778534	HI0024 homolog [Escherichia coli]	64	40
409	1	657	1607	gi|1773157	ferrochelatase [Escherichia coli]	64	41
446	1	266	775	gi|563845	orf gene product [Bacillus circulans]	64	53
462	4	1714	1959	gi|169461	serine proteinase inhibitor [Populus trichocarpa x Populus eltoides]	64	50
466	6	5621	8539	gi|143150	levR [Bacillus subtilis]	64	43
501	2	891	1469	gi|467109	rim; 30S Ribosomal protein S18 alanine acetyltransferase; 229_C1_170 [Mycobacterium leprae]	64	44
512	1	1	279	gi|1651948	hypothetical protein [Synechocystis sp.]	64	35
516	1	466	2	gi|155027	6'-N-acetyltransferase [Transposon Tn2426]	64	35
516	2	556	759	gi|1653387	nitrogen assimilation regulatory protein [Synechocystis sp.]	64	58
523	2	904	662	gi|159464	armadillo protein [Musca domestica]	64	45
537	2	1083	844	gi|929966	truncated ORFB due to a basepair deletion; similar to B. anthracis terneR element ORFB [Bacillus anthracis]	64	42
549	1	309	4	gi|1279769	FdhC [Methanobacterium thermoformicicum]	64	48
552	4	5960	3945	gi|1100076	PTS-dependent enzyme II [Clostridium longisporum]	64	47
556	1	3	224	gi|727437	putative 37-kDa protein [Lactococcus lactis]	64	49
557	2	767	1120	gnl|PID|e257629	transcription factor [Lactococcus lactis]	64	44
602	1	428	156	gi|520407	orf2; GTG start codon [Bacillus thuringiensis]	64	50
603	1	1	165	gi|1621445	sporulation protein Cse15 [Bacillus subtilis]	64	32

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
626	1	3	992	gi|1574715	thioredoxin reductase (trxB) [Haemophilus influenzae]	64	40
628	2	240	446	gi|1165281	Smg [Borrelia burgdorferi]	64	41
723	1	23	829	gi|1620648	surface protein Rib [Streptococcus agalactiae]	64	50
739	1	4	378	gi|143835	PBSX repressor [Bacillus subtilis]	64	37
748	1	139	765	gi|498816	ORF7; homology to regions 4.1 and 4.2 of sigma factors [Bacillus ubtilis]	64	35
758	1	3	410	gi|451201	ORF1 [Bacillus subtilis]	64	34
808	1	368	3	gi|142833	ORF2 [Bacillus subtilis]	64	47
818	2	415	663	gi|854020	U41, major DNA binding protein [Human herpesvirus 6]	64	40
906	1	2	433	gi|1303865	YqgR [Bacillus subtilis]	64	44
17	28	28175	27612	gi|151824	ORF5 [Plasmid R46]	63	34
19	18	9546	9722	gi|288661	ORF5 product [Bacteriophage P2]	63	45
39	5	1841	2329	gi|1573292	hypothetical [Haemophilus influenzae]	63	47
41	1	1531	2	gi|580896	nodB protein (aa 1-219) [Bradyrhizobium sp.]	63	43
55	10	5052	6410	gi|1303917	YqiB [Bacillus subtilis]	63	42
80	2	1852	824	gi|38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir|A29277|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus	63	42
81	10	6724	6221	gi|1591234	hypothetical protein (SP:P42297) [Methanococcus jannaschii]	63	40
81	14	9175	10848	gi|309662	pheromone binding protein [Plasmid pCF10]	63	44
86	1	2	1006	gi|143316	[gap] gene products [Bacillus megaterium]	63	43
89	13	12929	12639	gi|1377841	unknown [Bacillus subtilis]	63	44
98	14	14365	13502	sp|P45169|POTC_HAEIN	SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC.	63	37
100	24	20444	17985	gi|563258	virulence-associated protein E	63	44

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Dichelobacter nodosus]		
102	2	2441	2599	gi|1619835	MOB [Bacillus thuringiensis israelensis]	63	28
110	22	19725	20705	gi|1763011	lysophospholipase homolog [Homo sapiens]	63	48
115	1	481	92	gi|467360	unknown [Bacillus subtilis]	63	38
128	30	25257	24397	gi|1518679	orf [Bacillus subtilis]	63	39
138	18	12236	11580	gi|405516	This ORF is homologous to nitroreductase from Enterobacter cloacae, ccession Number A38686, and Salmonella, Accession Number P15888 Mycoplasma-like organism]	63	39
143	2	167	1096	pir|S39416|S39416	metallothionein 10-I - blue mussel	63	63
158	9	10023	8893	bbs|173803	CD4+ T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167, Peptide Partial, 268 aa] [Listeria monocytogenes]	63	48
164	6	3041	3301	gi|1573583	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	63	31
164	18	18502	21708	gi|1015903	ORF YJR151c [Saccharomyces cerevisiae]	63	45
165	3	3084	2278	gi|537108	ORF_f254 [Escherichia coli]	63	45
166	1	83	1045	gi|762778	NifS gene product [Anabaena azollae]	63	49
168	3	638	1489	gi|805022	Ndi1p [Saccharomyces cerevisiae]	63	32
171	12	10655	10810	gi|152403	phosphate regulatory protein [Rhizobium meliloti]	63	50
172	1	242	1336	gi|1552775	ATP-binding protein [Escherichia coli]	63	45
179	11	11236	12111	gnl|PID|e245033	unknown [Mycobacterium tuberculosis]	63	42
179	15	15289	15765	gi|1353197	thioredoxin reductase [Eubacterium acidaminophilum]	63	44
180	3	3412	1892	gi|1064813	homologous to sp:PHOR_BACSU [Bacillus subtilis]	63	40
180	7	7063	7926	gi|1657516	hypothetical protein [Escherichia coli]	63	41
187	1	1	729	gi|1651957	hypothetical protein [Synechocystis sp.]	63	34
195	17	7717	8280	gi|431928	MunI methyltransferase [Mycoplasma sp.]	63	44
202	8	5311	6165	gi|606162	ORF_f229 [Escherichia coli]	63	48

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
202	10	7848	8681	gi|606018	ORF_o783 [Escherichia coli]	63	47
208	3	2979	2341	gi|1006613	hypothetical protein [Synechocystis sp.]	63	40
221	3	874	1146	gnl|PID|e265530	yorfE [Streptococcus pneumoniae]	63	42
227	2	856	1254	gi|438459	homologous to E. coli hydrophobic Fe-uptake components FepD, FecD; utative [Bacillus subtilis]	63	41
231	3	2618	2448	gi|606248	30S ribosomal subunit protein S3 [Escherichia coli]	63	42
233	9	6773	6144	gi|887827	ORF_o192 [Escherichia coli]	63	41
234	1	348	70	gi|494958	ExpZ [Bacillus subtilis]	63	32
240	2	1230	721	gnl|PID|e252616	DcuC protein [Escherichia coli]	63	38
244	9	7512	6508	gi|467421	similar to B. subtilis DnaH [Bacillus subtilis] sp|P37540|YAAS_BACSU HYPOTHETICAL 37.6 KD PROTEIN IN XPAC-ABRB NTERGENIC REGION.	63	43
255	5	3600	2818	gi|1486244	unknown [Bacillus subtilis]	63	47
258	1	3	449	gi|1041115	TRAC [Plasmid pPD1]	63	38
259	4	2842	2342	gnl|PID|e290788	unknown [Mycobacterium tuberculosis]	63	42
265	8	3313	3480	gi|694074	emml gene product [Streptococcus pyogenes]	63	42
276	18	12505	11654	gi|601878	beta-1,3-glucanase bglH [Bacillus circulans]	63	36
294	5	2012	2275	gi|288661	ORF5 product [Bacteriophage P2]	63	40
301	7	7063	6704	gnl|PID|e290998	unknown [Mycobacterium tuberculosis]	63	41
345	2	2279	2725	gi|413940	ipa-16d gene product [Bacillus subtilis]	63	39
351	8	4361	3306	gi|398120	TDP-glucose oxireductase [Xanthomonas campestris]	63	47
359	1	526	14	gi|1001605	3-hydroxyisobutyrate dehydrogenase [Synechocystis sp.]	63	36
364	6	6741	7277	gi|1736473	ORF_ID:o335#13; similar to [SwissProt Accession Number P36088] [Escherichia coli]	63	42

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
378	2	683	1414	gi|529016	aminoglycoside 6-adenylyltransferase [Bacillus subtilis] pir|JU0059|XXBSG aminoglycoside 6-adenylyltransferase (EC 2.7.7.-) Bacillus subtilis	63	41
392	2	783	1646	gi|1772644	orfR gene product [Bacillus subtilis]	63	34
399	2	574	1407	gi|40023	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis] i|467388 stage III sporulation [Bacillus subtilis] ir|S18073|S18073 spoIIIJ protein - Bacillus subtilis	63	42
403	1	754	2	gi|1303938	YqiS [Bacillus subtilis]	63	52
404	5	4149	3745	gi|142450	ahrC protein [Bacillus subtilis]	63	42
430	1	2	1222	gi|1046082	M. genitalium predicted coding region MG372 [Mycoplasma genitalium]	63	40
432	1	3	1241	gi|1001328	UDP-MurNac-tripeptide synthetase [Synechocystis sp.]	63	33
432	4	1970	3016	gi|1161061	dioxygenase [Methylobacterium extorquens]	63	41
463	2	1324	851	gi|1573163	hypothetical [Haemophilus influenzae]	63	40
466	4	2843	3730	gnl|PID|e261988	putative ORF [Bacillus subtilis]	63	41
472	1	527	3	gi|556885	Unknown [Bacillus subtilis]	63	50
517	3	2803	1646	gi|531265	lipophilic protein which affects bacterial lysis rate and ethicillin resistance level [Staphylococcus aureus] pir|A55856|A55856 llm protein - Staphylococcus aureus	63	38
538	1	206	3	gi|172657	serine-protein kinase [Saccharomyces cerevisiae]	63	47
539	4	2997	3851	gi|973230	gamma-glutamyl kinase [Lycopersicon esculentum]	63	43
565	3	756	1010	gi|1303724	YqaF [Bacillus subtilis]	63	51
573	7	4518	3709	gi|1652352	dihydropteroate pyrophosphorylase [Synechocystis sp.]	63	45
579	2	361	1344	gi|1573114	beta-ketoacyl-acyl carrier protein	63	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					synthase III (fabH) [Haemophilus influenzae]		
593	2	390	1037	gi|409286	bmrU [Bacillus subtilis]	63	33
707	1	647	171	gi|511596	interleukin-2 [Canis familiaris]	63	33
714	1	2	268	gnl|PID|e213832	putative inner membrane protein [Bacillus licheniformis]	63	38
724	1	562	239	gnl|PID|e255315	unknown [Mycobacterium tuberculosis]	63	49
759	1	681	4	gi|437639	[Plasmodium falciparum 3' end.], gene product [Plasmodium alciparum]	63	28
794	1	981	313	gi|451201	ORF1 [Bacillus subtilis]	63	37
811	2	609	184	gi|150553	regulatory protein [Plasmid pCF10]	63	30
835	1	2	262	gi|1736496	RpiR protein. [Escherichia coli]	63	41
11	1	2	1144	gi|143150	levR [Bacillus subtilis]	62	48
12	5	8710	7673	gi|1486244	unknown [Bacillus subtilis]	62	43
15	3	1167	2957	gi|1592101	adenine deaminase [Methanococcus jannaschii]	62	40
16	4	2572	4092	gi|1109685	ProW [Bacillus subtilis]	62	37
23	4	1279	2067	gi|41432	fepC gene product [Escherichia coli]	62	35
23	26	16176	16454	gi|154499	carbon dioxide concentrating mechanism protein [Synechococcus sp.] pir|C36904|C36904 carbon dioxide concentrating mechanism protein cmL - Synechococcus sp. (PCC 7942)	62	41
31	6	5322	5774	gi|532309	25 kDa protein [Escherichia coli]	62	38
68	4	1606	2778	gi|1732203	GlcNAc 6-P deacetylase [Vibrio furnissii]	62	44
72	1	1	540	gi|1573097	glucosamine-6-phosphate deaminase protein (nagB) [Haemophilus influenzae]	62	26
76	3	1937	2227	gi|928830	ORF75; putative [Lactococcus lactis phage BK5-T]	62	34
83	16	11700	12272	gi|1592161	N-terminal acetyltransferase complex, subunit ARD1 [Methanococcus jannaschii]	62	33

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
83	19	12685	13737	gi|1653193	sialoglycoprotease [Synechocystis sp.]	62	42
91	6	3232	3789	gi|1762962	FemA [Staphylococcus simulans]	62	37
100	43	29676	29317	gi|963033	orf1 gene product [Enterococcus hirae]	62	45
101	8	7410	6481	gi|1161061	dioxygenase [Methylobacterium extorquens]	62	45
110	3	653	871	gi|992683	mdm2-D [Homo sapiens]	62	37
110	8	8440	5810	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	62	46
111	2	1057	287	gnl|PID|e253280	ORF YDL238c [Saccharomyces cerevisiae]	62	45
114	5	6886	7662	gi|152719	flavocytochrome c [Shewanella putrefaciens]	62	37
115	4	1401	1994	gi|1303978	YqkA [Bacillus subtilis]	62	46
118	1	545	225	gi|39431	oligo-1,6-glucosidase [Bacillus cereus]	62	40
119	8	4625	4356	gi|1522673	type I restriction enzyme [Methanococcus jannaschii]	62	33
120	2	257	1270	gnl|PID|e235823	unknown [Schizosaccharomyces pombe]	62	41
121	8	7543	8034	gi|39475	formamidopyrimidine-DNA glycosylase [Bacillus firmus] ir|S11489|S11489 formamidopyrimidine-DNA glycosidase (EC 3.2.2.23) Bacillus firmus	62	48
123	2	1677	592	gi|882252	conjugated bile acid hydrolase [Clostridium perfringens] sp|P54965|CBH_CLOPE CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) CONJUGATED BILE ACID HYDROLASE) (CBAH) (BILE SALT HYDROLASE).	62	40
128	16	10895	9408	gi|1742834	PTS system, cellobiose-specific IIC component (EIIC-CEL) (Cellobiose- permease IIC component) (Phosphotransferase enzyme II, C component). [Escherichia coli]	62	43

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
128	29	24254	23544	gi|1518680	minicell-associated protein DivIVA [Bacillus subtilis]	62	37
128	35	28843	28103	gi|142940	ftsA [Bacillus subtilis]	62	42
133	4	3434	4165	gnl|PID|e235174	unknown [Mycobacterium tuberculosis]	62	38
134	2	1679	933	gi|155032	ORF B [Plasmid pEa34]	62	36
146	6	4923	4651	gi|153675	tagatose 6-P kinase [Streptococcus mutans]	62	48
149	5	3318	2527	gi|1591587	pantothenate metabolism flavoprotein [Methanococcus jannaschii]	62	35
152	9	4830	5747	gi|1652461	lactose transport system permease protein LacF [Synechocystis sp.]	62	39
163	2	1341	544	gi|533098	DnaD protein [Bacillus subtilis]	62	41
164	14	9567	9322	gi|1118060	coded for by C. elegans cDNA yk3d11.5; coded for by C. elegans cDNA yk5f4.5 [Caenorhabditis elegans]	62	27
172	8	6613	7146	gi|915199	ggaB [Bacillus subtilis]	62	33
173	13	11127	9736	gi|1653484	hypothetical protein [Synechocystis sp.]	62	44
177	1	1077	364	gi|1572994	2-keto-3-deoxy-6-phosphogluconate aldolase (eda) [Haemophilus influenzae]	62	38
178	4	1683	1318	gnl|PID|e155310	Orf2 [Bacteriophage TP901-1]	62	51
179	5	6425	7576	gi|1161933	DltB [Lactobacillus casei]	62	44
180	13	12470	10842	sp|P37047|YAEG_ECOLI	HYPOTHETICAL 44.3 KD PROTEIN IN HTRA-DAPD INTERGENIC REGION.	62	38
181	14	11649	10735	gi|1742758	Shikimate 5-dehydrogenase (EC 1.1.1.25). [Escherichia coli]	62	41
197	2	516	1442	gi|623476	transcriptional activator [Providencia stuartii] sp|P43463|AARP_PROST TRANSCRIPTIONAL ACTIVATOR AARP.	62	34
206	5	2728	1790	gnl|PID|e265638	unknown [Mycobacterium tuberculosis]	62	37
210	2	938	2290	gi|528991	unknown [Bacillus subtilis]	62	41
221	15	7083	7280	gnl|PID|e219154	K08F4.5 [Caenorhabditis elegans]	62	44
222	11	7141	8022	gi|537034	ORF_o488 [Escherichia coli]	62	39

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
223	9	6924	6358	gnl|PID|e283128	unknown, highly similar to E. coli YecD hypothtical 21.8 KD protein in aspS 5'region and to isochorismatase [Bacillus subtilis]	62	42
225	4	2055	2885	gi|18724	pyrroline-5-carboxylate reductase (AA 1-274) [Glycine max] ir|S10186|S10186 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - ybean	62	39
229	11	11428	10670	gnl|PID|e235745	hypothetical protein [Mycobacterium leprae]	62	36
231	1	1244	3	gi|48808	dciAE gene product [Bacillus subtilis]	62	45
233	1	801	4	gi|143391	ORF2 [Bacillus subtilis]	62	42
233	13	10471	9431	gi|887825	ORF_f541 [Escherichia coli]	62	35
242	1	3	149	gi|532549	ORF16 [Enterococcus faecalis]	62	44
255	2	443	1009	gi|639789	ORF9 [Mycoplasma pneumoniae]	62	44
266	6	2349	2158	gnl|PID|e194945	yeast sds22 homolog [Homo sapiens]	62	37
270	1	3	314	gi|1303827	YqfI [Bacillus subtilis]	62	35
270	7	5136	4447	gi|1303958	YqjG [Bacillus subtilis]	62	41
279	1	271	2	gnl|PID|e185372	ceuC gene product [Campylobacter coli]	62	44
301	11	9598	8798	gi|1303863	YqgP [Bacillus subtilis]	62	45
306	2	750	1202	gi|148771	ribosomal protein HmaS4 [Haloarcula marismortui]	62	41
308	3	2328	1684	gnl|PID|e238666	hypothetical protein [Bacillus subtilis]	62	40
309	5	8806	8573	gi|1591861	M. jannaschii predicted coding region MJ1230 [Methanococcus jannaschii]	62	37
318	3	2278	1283	gi|1256134	YbbE [Bacillus subtilis]	62	37
321	3	1433	1792	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli]	62	37
338	13	11175	12770	gi|467446	similar to SpoVB [Bacillus subtilis]	62	38
345	11	10519	11793	gi|1736789	Collagenase precursor (EC 3.4.-.-).	62	40

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Escherichia coli]		
345	21	22459	22947	gi|1657794	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase [Methylobacterium extorquens]	62	47
358	1	902	36	gi|409241	penicillin-binding protein 2 [Staphylococcus aureus]	62	44
362	6	2930	3493	gnl|PID|e255091	hypothetical protein [Bacillus subtilis]	62	37
363	2	3242	1581	gnl|PID|e254997	hypothetical protein [Bacillus subtilis]	62	40
365	2	400	1770	gi|143150	levR [Bacillus subtilis]	62	42
372	5	2525	4489	gi|1045736	fructose-permease IIBC component [Mycoplasma genitalium]	62	43
373	1	3	851	gi|438462	transmembrane protein [Bacillus subtilis]	62	36
375	1	2	1336	gi|732813	branched-chain amino acid carrier [Lactobacillus delbrueckii] pir|S60180|S60180 branched-chain amino acid carrier brnQ - actobacillus delbrueckii	62	43
375	3	2592	1831	gi|1644206	unknown [Bacillus subtilis]	62	43
391	2	142	510	gi|151776	ORF3 [Escherichia coli]	62	31
396	2	254	1051	gi|410131	ORFX7 [Bacillus subtilis]	62	41
423	1	197	6	pir|A33592|A33592	repressor protein catM - Acinetobacter calcoaceticus	62	38
436	1	704	3	gi|455376	unidentified reading frame L (ORFL) (putative); putative [Transposon n10]	62	32
466	8	9320	10480	gi|147402	mannose permease subunit III-Man [Escherichia coli]	62	44
488	5	2175	2927	gi|532546	ORF13 [Enterococcus faecalis]	62	40
510	4	2572	3078	gi|43941	EIII-B Sor PTS [Klebsiella pneumoniae]	62	35
517	2	1533	736	gi|559388	epsX gene product [Acinetobacter calcoaceticus]	62	53
519	1	2	1084	gi|1652876	hypothetical protein [Synechocystis sp.]	62	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
535	1	353	69	gi|1196922	unknown protein [Insertion sequence IS861]	62	33
579	1	1	363	gi|535052	involved in protein secretion [Bacillus subtilis]	62	22
656	5	5351	5956	gnl|PID|e290931	unknown [Mycobacterium tuberculosis]	62	40
666	1	445	128	gi|483940	transcription regulator [Bacillus subtilis]	62	42
682	1	597	172	gi|146724	enzyme III-Man function protein (manX (ptsL)) [Escherichia coli] gi|41976 manX gene product (AA 1-315) [Escherichia coli]	62	37
771	1	3	365	gi|1773086	similar to S. typhimurium ProY [Escherichia coli]	62	44
831	1	390	94	gnl|PID|e255000	hypothetical protein [Bacillus subtilis]	62	55
15	5	4421	5260	gnl|PID|e214719	PlcR protein [Bacillus thuringiensis]	61	38
16	6	4705	4938	gi|758425	complement component C3 [Xenopus laevis/gilli]	61	44
23	16	10279	11214	sp|P19265|EUTC_SALTY	ETHANOLAMINE AMMONIA-LYASE LIGHT CHAIN (EC 4.3.1.7).	61	46
33	2	1789	2205	gi|413958	ipa-34d gene product [Bacillus subtilis]	61	36
33	5	4756	6594	gi|1001823	cadmium-transporting ATPase [Synechocystis sp.]	61	38
37	4	2813	3295	gi|1256140	YbbK [Bacillus subtilis]	61	51
37	7	5973	5215	gnl|PID|e269488	Unknown [Bacillus subtilis]	61	33
49	4	1567	1839	gnl|PID|e139445	major tail protein [Bacteriophage B1]	61	43
56	1	108	641	gi|1574067	H. influenzae predicted coding region HI1034 [Haemophilus influenzae]	61	35
59	1	1	1002	gi|763513	ORF4; putative [Streptomyces violaceoruber]	61	37
69	7	4837	5523	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	61	34
72	11	9262	10476	gi|1591272	ferrous iron transport protein B [Methanococcus jannaschii]	61	45
83	2	731	1549	gi|755152	highly hydrophobic integral membrane	61	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					protein [Bacillus subtilis] sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.		
87	2	2067	925	gi|1573129	hypothetical [Haemophilus influenzae]	61	46
103	5	2689	3495	gi|1685111	orf1091 [Streptococcus thermophilus]	61	45
110	13	11455	11820	gi|1001825	transcriptional repressor SmtB [Synechocystis sp.]	61	42
110	15	14048	12588	gi|1573583	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	61	38
111	3	1675	1055	gnl|PID|e253280	ORF YDL238c [Saccharomyces cerevisiae]	61	34
111	4	1838	2518	gi|1574513	hypothetical [Haemophilus influenzae]	61	50
111	5	2535	3158	gi|537235	Kenn Rudd identifies as gpmB [Escherichia coli]	61	40
121	1	3	1397	gi|290643	ATPase [Enterococcus hirae]	61	50
123	28	25608	27734	gi|143150	levR [Bacillus subtilis]	61	39
125	5	3455	2589	gi|148921	LicD protein [Haemophilus influenzae]	61	47
128	14	9382	9146	gi|575361	protein kinase PkpA [Phycomyces blakesleeanus]	61	38
138	32	23151	21628	gi|1184262	GadC [Shigella flexneri]	61	34
144	8	6311	5325	gi|710422	cmp-binding-factor 1 [Staphylococcus aureus]	61	39
171	4	4601	5566	gi|41500	ORF 3 (AA 1-352); 38 kD (put. ftsX) [Escherichia coli]	61	31
172	3	2006	2848	gi|303560	ORF271 [Escherichia coli]	61	42
173	7	5146	6228	gi|1256134	YbbE [Bacillus subtilis]	61	31
197	8	9183	8182	gi|143803	GerC3 [Bacillus subtilis]	61	33
217	5	3007	3462	gi|1749414	unnamed protein product [Schizosaccharomyces pombe]	61	43
217	8	6099	5464	gi|143456	rpoE protein (ttg start codon) [Bacillus subtilis]	61	37
222	6	3400	3927	gnl|PID|e255118	hypothetical protein [Bacillus subtilis]	61	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
225	3	1946	981	gi|1574660	xylose operon regluatory protein (xylR) [Haemophilus influenzae]	61	43
237	2	203	952	gi|1019108	alternate start at bp 59; ORF [Bacteriophage phi-80]	61	52
237	7	3058	3279	gnl|PID|e246904	ORF YPL169c [Saccharomyces cerevisiae]	61	32
262	1	20	913	gnl|PID|e214719	PlcR protein [Bacillus thuringiensis]	61	35
271	17	12725	13504	gi|143057	ORF39 [Bacillus subtilis]	61	31
275	8	5370	3697	gi|1542975	AbcB [Thermoanaerobacterium thermosulfurigenes]	61	41
280	2	692	3079	gi|1001352	ABC transporter [Synechocystis sp.]	61	42
294	7	2276	2767	gi|662792	single-stranded DNA binding protein [unidentified eubacterium]	61	44
301	12	9965	9519	gi|1303861	YqgN [Bacillus subtilis]	61	41
308	1	1471	26	gi|1276882	EpsI [Streptococcus thermophilus]	61	36
314	2	475	1662	gi|975351	PatB [Bacillus subtilis]	61	42
321	9	3762	4193	gi|1732202	PTS permease for mannose subunit IIIMan N terminal domain [Vibrio furnissii]	61	40
323	5	5118	5537	gi|532540	ORF7 [Enterococcus faecalis]	61	28
324	7	4800	5156	gi|146122	H-protein [Escherichia coli]	61	39
338	3	1456	1989	pir|A47071|A47071	orf1 immediately 5' of nifS - Bacillus subtilis	61	43
341	2	342	947	gi|1736577	Octopine transport system permease protein OccM. [Escherichia coli]	61	41
349	3	1788	1363	pir|G64143|G64143	hypothetical protein HI0143 - Haemophilus influenzae (strain Rd KW20)	61	38
369	2	1261	587	gi|153744	ORF X; putative [Streptococcus mutans]	61	33
371	2	1801	1562	gi|48836	xylulokinase [Staphylococcus xylosus]	61	40
372	4	1575	2543	gi|149395	lacC [Lactococcus lactis]	61	43
379	11	12683	11727	gi|887829	D21141 uses 2nd start; frame determined by Lac fusion [Escherichia oli]	61	40
383	5	5625	3820	gi|624072	similar to Escherichia coli	61	36

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					glycerophosphoryl diester hosphodiesterase, Swiss-Prot Accession Number P10908 [Paramecium ursaria Chlorella virus 1]		
395	2	771	517	gnl|PID|e276251	T23G11.6 [Caenorhabditis elegans]	61	42
399	20	15621	15812	gi|472527	protein phosphatase 1 [Schizosaccharomyces pombe]	61	44
413	1	3	749	gnl|PID|e289144	ywpE [Bacillus subtilis]	61	42
427	1	1079	288	gi|403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	61	42
436	4	2045	1761	gi|48669	pot. ORF B [Shigella sonnei]	61	38
437	1	1158	244	gi|580866	ipa-12d gene product [Bacillus subtilis]	61	47
482	2	1676	1167	bbs|158786	4A11 antigen, sperm tail membrane antigen=putative sucrose-specific phosphotransferase enzyme II homolog [mice, testis, Peptide Partial, 172 aa] [Mus sp.]	61	42
490	3	1291	1094	gnl|PID|e248473	putative phosphate permease [Arabidopsis thaliana]	61	35
514	1	687	142	gi|1742775	msm operon regulatory protein. [Escherichia coli]	61	36
541	1	758	3	gi|1591732	cobalt transport ATP-binding protein O [Methanococcus jannaschii]	61	39
551	3	2163	1600	gi|671632	unknown [Staphylococcus aureus]	61	38
603	2	163	564	gi|1408587	relaxase [Lactococcus lactis lactis]	61	39
637	8	4539	4769	gi|143559	subtilin [Bacillus subtilis]	61	38
765	1	34	681	gi|408888	orfA 5' of intG [Lactobacillus bacteriophage phi adh] pir|PN0468|PN0468 hypothetical protein 106 - Lactobacillus	61	40

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					gasseri fragment)		
773	1	53	1207	gi|143841	xylose repressor [Bacillus subtilis]	61	36
798	1	175	381	gi|187572	located at OATL1 [Homo sapiens]	61	32
5	2	303	998	gi|1783264	homologous to DNA glycosylases; hypothetical [Bacillus subtilis]	60	50
8	8	5891	6550	gi|1777939	Pfs [Treponema pallidum]	60	40
11	7	4096	4935	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	60	41
11	8	4919	5254	gi|467125	glmS; L-Glucosamine:D-fructose-6-phosphate aminotransferase; 229_C3_238 [Mycobacterium leprae]	60	30
17	9	7736	8203	gi|496514	orf zeta [Streptococcus pyogenes]	60	42
20	1	3	443	gi|861137	chitin binding protein [Streptomyces olivaceoviridis] pir|S55001|S55001 CHB1 protein - Streptomyces olivaceoviridis (SUB -30)	60	40
21	3	1970	684	gi|1778520	hypothetical protein [Escherichia coli]	60	43
23	11	5357	5953	gi|619066	NAST [Azotobacter vinelandii]	60	31
34	4	6662	3279	gi|153952	polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] pir|A45915|A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III lpha chain - Salmonella typhimurium	60	37
39	1	47	466	gi|1561567	Unknown [Bacillus subtilis]	60	35
39	4	1855	1361	gi|298045	Orf154 [Streptomyces ambofaciens]	60	41
48	4	2554	4128	gi|1255259	o-succinylbenzoic acid (OSB) CoA ligase [Staphylococcus aureus]	60	40
56	9	6682	5795	gi|413940	ipa-16d gene product [Bacillus subtilis]	60	40
65	3	2105	2593	gi|1573061	hypothetical [Haemophilus influenzae]	60	34
72	9	7854	8330	gi|606343	CG Site No. 28964 [Escherichia coli]	60	39
81	3	2053	1406	gi|1574770	phenylalanyl-tRNA synthetase beta-subunit (pheT) [Haemophilus influenzae]	60	46

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
81	4	2987	2130	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	60	34
81	12	8280	7150	gnl|PID|e254984	hypothetical protein [Bacillus subtilis]	60	44
83	22	16887	16537	gi|509672	repressor protein [Bacteriophage Tuc2009]	60	33
89	1	698	60	gi|840838	hypothetical 21.7 kDa protein in ftsY 5' region [Pseudomonas eruginosa]	60	36
89	12	12641	11856	gi|1377843	unknown [Bacillus subtilis]	60	40
89	17	18879	15844	gi|666069	orf2 gene product [Lactobacillus leichmannii]	60	37
94	6	2281	3384	gi|468760	ORF334 [Rhizobium meliloti]	60	36
98	1	12	1970	gi|1652892	ABC transporter [Synechocystis sp.]	60	38
99	3	978	1460	gi|473955	DNA-binding protein [Lactobacillus sp.]	60	31
100	35	26818	26333	gi|347851	junctional sarcoplasmic reticulum glycoprotein [Oryctolagus uniculus]	60	48
100	45	30072	30449	gi|143547	Sin regulatory protein (ttg start codon) [Bacillus subtilis] gi|1303886 SinR [Bacillus subtilis]	60	43
102	8	5923	6561	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	60	25
109	1	362	3	pir|S10655|S10655	hypothetical protein X - Pyrococcus woesei (fragment)	60	33
110	16	14806	14087	pir|JH0364|JH0364	hypothetical protein 176 (SAGP 5' region) - Streptococcus pyogenes	60	35
110	20	18929	18414	gi|142450	ahrC protein [Bacillus subtilis]	60	39
110	21	19124	19624	gi|142450	ahrC protein [Bacillus subtilis]	60	40
111	1	289	2	gi|1256618	transport protein [Bacillus subtilis]	60	31
122	7	5627	9589	gi|217191	5'-nucleotidase precursor [Vibrio parahaemolyticus]	60	39
123	5	4390	3659	gi|1197667	vitellogenin [Anolis pulchellus]	60	27
123	20	18102	18407	gi|1303705	YrkF [Bacillus subtilis]	60	34

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
128	32	26229	25492	gi|1652485	hypothetical protein [Synechocystis sp.]	60	29
129	5	4421	6259	gi|1303853	YqgF [Bacillus subtilis]	60	36
131	2	1112	2338	gi|699112	ugpC gene product [Mycobacterium leprae]	60	41
131	4	3194	4036	gi|296356	putative membrane transport protein [Clostridium perfringens] pir|A56641|A56641 probable membrane transport protein - Clostridium erfringens	60	32
131	8	6669	7901	gi|537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli] pir|S56438|S56438 2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC .1.4.16) - Escherichia coli	60	40
133	11	9854	10240	gnl|PID|e249654	YneR [Bacillus subtilis]	60	37
138	7	6793	6263	gi|1486247	unknown [Bacillus subtilis]	60	48
146	4	2831	2328	gi|39979	P18 [Bacillus subtilis]	60	38
149	6	3504	3316	gi|145173	35 kDa protein [Escherichia coli]	60	47
154	5	2599	3558	gi|1773109	similar to S. typhimurium apbA [Escherichia coli]	60	41
155	5	3061	4701	gi|388269	traC [Plasmid pAD1]	60	38
155	11	8565	8927	gi|1197460	MtfB [Escherichia coli]	60	39
158	10	11123	10032	gi|581809	tmbC gene product [Treponema pallidum]	60	39
165	7	6131	5700	gi|1439527	EIIA-man [Lactobacillus curvatus]	60	35
172	4	3169	3810	gi|1001342	hypothetical protein [Synechocystis sp.]	60	42
174	2	1574	762	gi|1045808	hypothetical protein (GB:U00021_19) [Mycoplasma genitalium]	60	35
181	7	4975	4460	gi|683584	shikimate kinase [Lactococcus lactis]	60	33
183	6	2719	2955	gi|1146198	ferredoxin [Bacillus subtilis]	60	37
189	2	3528	2221	gi|396301	matches PS00041: Bacterial regulatory proteins, araC family ignature [Escherichia coli]	60	35
193	5	3121	2600	gi|39788	adaB [Bacillus subtilis]	60	49

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
195	11	4623	6569	gnl|PID|e250887	potential coding region [Clostridium difficile]	60	39
202	2	1837	1607	gi|693939	membrane ATPase [Haloferax volcanii]	60	32
206	7	4794	3754	gi|1574702	hypothetical [Haemophilus influenzae]	60	42
209	2	1308	433	pir|A38587|A38587	collagen, corneal - chicken (fragment)	60	51
220	3	4263	1213	gi|437706	alternative truncated translation product from E.coli [Streptococcus neumoniae]	60	41
222	9	6019	6522	gi|882463	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia oli]	60	47
222	12	8001	8336	gi|537035	ORF_o101 [Escherichia coli]	60	33
233	2	1294	827	gi|145091	flavodoxin [Desulfovibrio salexigens]	60	39
242	11	7370	7627	gi|1353404	cytochrome oxidase subunit I [Metridium senile]	60	28
249	3	1109	1768	gi|143156	membrane bound protein [Bacillus subtilis]	60	41
251	3	4053	1933	gi|1235662	RfbC [Myxococcus xanthus]	60	42
256	4	2614	3867	gi|532612	ecotropic retrovirus receptor [Mus musculus]	60	37
260	2	1539	802	gi|1208447	metalloprotease transporter [Serratia marcescens]	60	35
261	5	4528	3179	gnl|PID|e246728	histidine kinase [Streptococcus gordonii]	60	25
269	3	2723	1563	gi|1591618	M. jannaschii predicted coding region MJ0951 [Methanococcus jannaschii]	60	39
269	4	3541	2780	gi|1303794	YqeM [Bacillus subtilis]	60	36
269	11	7164	6595	gi|1303787	YqeG [Bacillus subtilis]	60	38
271	2	677	1651	gnl|PID|e269877	riboflavin kinase [Bacillus subtilis]	60	43
271	3	1639	2247	gi|537148	ORF_f181 [Escherichia coli]	60	41
271	18	13502	13762	pir|S39341|S39341	grpE protein - Lactococcus lactis	60	40
277	2	1662	979	gi|1773109	similar to S. typhimurium apbA [Escherichia coli]	60	41
279	13	10627	9773	gi|290545	f270 [Escherichia coli]	60	41
290	2	790	1695	gi|152886	elongation factor Ts (tsf) [Spiroplasma	60	38

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					citri]		
291	4	3571	2612	gnl|PID|e257610	sugar-binding transport protein [Anaerocellum thermophilum]	60	40
295	3	1309	2094	gi|1000453	TreR [Bacillus subtilis]	60	37
301	15	11063	11344	gi|535274	ORF1 [Streptococcus thermophilus]	60	36
310	3	2903	1266	gi|809765	aspartate aminotransferase (AA 1-402) [Sulfolobus solfataricus] pir|S07088|S07088 aspartate transaminase (EC 2.6.1.1) - Sulfolobus olfataricus	60	44
316	2	319	119	bbs|115298	polyprotein(coat protein) [raspberry ringspot virus RRV, Peptide, 1107 aa] [Raspberry ringspot virus]	60	28
320	4	3085	2483	gi|143002	proton glutamate symport protein [Bacillus caldotenax] pir|S26246|S26246 glutamate/aspartate transport protein - Bacillus aldotenax	60	26
323	1	1	681	gi|1477486	transposase [Burkholderia cepacia]	60	44
330	4	3361	4488	gi|1778517	glycerol dehydrogenase homolog [Escherichia coli]	60	48
356	3	2471	2205	gi|57633	neuronal myosin heavy chain [Rattus rattus]	60	40
362	5	2458	2925	gnl|PID|e255090	hypothetical protein [Bacillus subtilis]	60	36
364	4	4096	5349	gi|1657522	hypothetical protein [Escherichia coli]	60	41
383	1	654	4	gnl|PID|e288399	F56H6.k [Caenorhabditis elegans]	60	39
383	2	2208	853	gi|143536	sigma factor 54 [Bacillus subtilis]	60	37
386	2	130	510	gi|1046053	hypothetical protein (SP:P32049) [Mycoplasma genitalium]	60	42
399	26	25892	27757	gi|895747	putative cel operon regulator [Bacillus subtilis]	60	30
399	27	27721	28239	gi|146281	gut operon activator (gutM) [Escherichia coli]	60	35
401	4	2081	3523	gi|142833	ORF2 [Bacillus subtilis]	60	36

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
405	2	1353	763	gi|633113	ORF3 [Streptococcus sobrinus]	60	42
407	7	4380	4589	gi|1674126	(AE000043) Mycoplasma pneumoniae, MG280 homolog, from M. genitalium [Mycoplasma pneumoniae]	60	39
408	1	12	539	gi|455006	orf6 [Rhodococcus fascians]	60	42
421	7	4113	3925	gi|60020	ORF31 (AA1-868) [Human herpesvirus 3]	60	43
452	3	712	2223	gi|532554	ORF21 [Enterococcus faecalis]	60	38
462	3	2066	1551	gi|1015903	ORF YJR151c [Saccharomyces cerevisiae]	60	37
480	1	12	272	gi|468715	sss gene product [Pseudomonas aeruginosa]	60	34
487	1	1091	3	gi|388269	traC [Plasmid pAD1]	60	39
490	5	2108	1479	gi|699379	glvr-1 protein [Mycobacterium leprae]	60	29
507	1	221	751	gi|1303952	YqjA [Bacillus subtilis]	60	37
511	1	449	63	gi|391610	farnesyl diphosphate synthase [Bacillus stearothermophilus] pir|JX0257|JX0257 geranyltranstransferase (EC 2.5.1.10) - Bacillus tearothermophilus	60	42
551	2	1521	604	gi|1256648	putative [Bacillus subtilis]	60	37
552	1	887	63	gi|537235	Kenn Rudd identifies as gpmB [Escherichia coli]	60	40
610	1	1	792	gi|1321625	exo-alpha-1, 4-glucosidase [Bacillus stearothermophilus]	60	45
642	1	402	214	gi|992964	thioredoxin [Arabidopsis thaliana]	60	36
646	1	642	265	gi|1041115	TRAC [Plasmid pPD1]	60	32
661	2	305	943	gi|1651536	3-oxoacyl-[acyl-carrier-protein] reductase [Escherichia coli]	60	37
678	1	536	3	gi|532554	ORF21 [Enterococcus faecalis]	60	39
716	1	799	305	gi|886040	ORFtxe1 [Clostridium difficile]	60	38
717	1	2	472	gi|1402529	ORF8 [Enterococcus faecalis]	60	31
727	1	516	82	gi|471283	ORF [Synechococcus PCC6301]	60	41
770	1	327	4	gi|467451	unknown [Bacillus subtilis]	60	33
843	1	234	4	gi|2819	transferase (GAL10) (AA 1 - 687)	60	37

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Kluyveromyces lactis] r|S01407|XUVKG UDPglucose 4-epimerase (EC 5.1.3.2) - yeast uyveromyces marxianus var. lactis)		
21	1	341	3	gi|1778519	hypothetical protein [Escherichia coli]	59	47
23	2	290	1303	gi|1407800	ABC-type permease [Yersinia pestis]	59	36
23	13	6720	7388	gi|1652472	ethylene response sensor protein [Synechocystis sp.]	59	37
23	18	11892	12413	gi|825627	major carboxysome shell protein [Thiobacillus neapolitanus] pir|S60136|S60136 major carboxysome shell protein - Thiobacillus eapolitanus	59	42
29	4	1989	2852	gi|1742383	ORF_ID:o276#3; similar to [PIR Accession Number S11432] [Escherichia coli]	59	48
32	8	4504	4064	gi|1046081	hypothetical protein (GB:D26185_10) [Mycoplasma genitalium]	59	33
37	9	6670	6284	gi|290561	o188 [Escherichia coli]	59	44
47	1	2	2743	gnl|PID|e248792	unknown [Mycobacterium tuberculosis]	59	46
48	5	4017	5492	gi|1185288	isochorismate synthase [Bacillus subtilis]	59	40
49	5	1797	2093	gi|496280	structural protein [Bacteriophage Tuc2009]	59	41
59	8	3324	5057	gi|1486244	unknown [Bacillus subtilis]	59	35
72	14	13937	13434	gi|532540	ORF7 [Enterococcus faecalis]	59	25
81	20	14659	14219	gi|39978	P16 [Bacillus subtilis]	59	38
98	2	1961	2617	gi|41519	P30 protein (AA 1-240) [Escherichia coli]	59	39
102	3	2542	3774	gi|1674376	(AE000062) Mycoplasma pneumoniae, MG148 homolog, from M. genitalium [Mycoplasma pneumoniae]	59	30
116	2	907	1458	gi|1146225	putative [Bacillus subtilis]	59	37
116	7	3532	4842	gi|1146238	poly(A) polymerase [Bacillus subtilis]	59	41
128	20	15626	14310	gi|1001719	ATP-dependent RNA helicase DeaD [Synechocystis sp.]	59	34
134	4	3158	3850	gi|1477486	transposase [Burkholderia cepacia]	59	40

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
137	1	1	999	gi|1065948	similar to thymidine diphosphoglucose 4,6-dehydratase [Caenorhabditis elegans]	59	40
138	8	7489	6827	gnl|PID|e264435	Putative orf YCLX8c, len:192 [Saccharomyces cerevisiae]	59	36
140	1	3	656	gnl|PID|e254943	unknown [Mycobacterium tuberculosis]	59	32
165	13	10427	9849	gi|1732199	PTS permease for mannose subunit IIIMan C terminal domain [Vibrio furnissii]	59	37
167	1	2	1045	gi|1573128	hypothetical [Haemophilus influenzae]	59	38
173	2	430	2160	gi|1486244	unknown [Bacillus subtilis]	59	31
179	10	10432	11199	gi|288299	ORF1 gene product [Bacillus megaterium]	59	34
179	12	12117	13148	gi|1045964	hypothetical protein (GB:U14003_297) [Mycoplasma genitalium]	59	41
181	11	9684	8575	gi|1653152	3-dehydroquinate synthase [Synechocystis sp.]	59	41
223	24	20736	21974	gi|1573051	succinyl-diaminopimelate desuccinylase (dapE) [Haemophilus influenzae]	59	48
229	12	12818	11421	gi|1652035	fmu and fmv protein [Synechocystis sp.]	59	39
244	3	2836	1565	gi|1303959	YqjH [Bacillus subtilis]	59	45
265	9	4116	3868	gi|311100	translational activator [Saccharomyces cerevisiae]	59	28
272	1	1	546	gi|490320	Y gene product [unidentified]	59	41
279	16	14774	14370	gi|1389549	ORF3 [Bacillus subtilis]	59	46
283	8	3222	3401	gi|153047	lysostaphin (ttg start codon) [Staphylococcus simulans] pir|A25881|A25881 lysostaphin precursor - Staphylococcus simulans sp|P10547|LSTP_STASI LYSOSTAPHIN PRECURSOR (EC 3.5.1.-).	59	43
288	5	2617	3144	gi|1142714	phosphoenolpyruvate:mannose phosphotransferase element IIB [Lactobacillus curvatus]	59	45
292	19	14837	16792	gi|495646	ATPase [Transposon Tn5422]	59	40

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
295	1	49	495	gi|533098	DnaD protein [Bacillus subtilis]	59	39
315	2	907	653	gi|1574802	hypothetical [Haemophilus influenzae]	59	38
318	6	4549	4058	gi|43941	EIII-B Sor PTS [Klebsiella pneumoniae]	59	35
345	3	2707	3507	gi|895749	putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis]	59	38
351	5	2646	2371	gi|1666506	RfbC [Leptospira interrogans]	59	30
355	21	15237	17222	gi|515738	ORF2; putative [Oenococcus oeni]	59	35
384	1	14	754	gi|1162959	homologous to HI0365 in Haemophilus influenzae; ORF1 [Pseudomonas aeruginosa]	59	34
385	1	3	533	gi|1146197	putative [Bacillus subtilis]	59	36
394	13	13137	12160	gnl|PID|e243582	ORF YGR263c [Saccharomyces cerevisiae]	59	36
399	1	224	580	gi|580904	homologous to E.coli rnpA [Bacillus subtilis]	59	38
412	1	3	2927	gi|1620648	surface protein Rib [Streptococcus agalactiae]	59	43
412	2	2918	3559	gi|1620648	surface protein Rib [Streptococcus agalactiae]	59	43
416	6	5283	3940	gi|1100076	PTS-dependent enzyme II [Clostridium longisporum]	59	38
437	2	1561	1136	gi|580866	ipa-12d gene product [Bacillus subtilis]	59	44
495	2	438	614	gi|1500472	M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]	59	45
502	1	853	188	gi|1063248	No homologous protein [Bacillus subtilis]	59	25
573	8	5092	4493	gi|1573226	hypothetical [Haemophilus influenzae]	59	39
579	4	1716	2717	gnl|PID|e280724	unknown [Mycobacterium tuberculosis]	59	41
600	1	1	504	gi|49386	internal region of the penicillin-binding protein 2B gene treptococcus pneumoniae]	59	40
616	3	904	533	gi|289265	[Bacillus sp. (KSM 64) endo-1,4-beta-glucanase gene, complete cds.], ene products [Bacillus sp.]	59	44
657	1	432	4	gi|1651338	PnuC protein [Escherichia coli]	59	37

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
699	1	416	165	gnl|PID|e199096	PepR1 [Lactobacillus delbrueckii]	59	23
713	4	3709	2660	gi|515738	ORF2; putative [Oenococcus oeni]	59	37
715	1	698	84	gi|1176399	EpiF [Staphylococcus epidermidis]	59	42
737	2	660	199	gi|666000	hypothetical protein [Bacillus subtilis]	59	43
744	1	395	3	gi|1732057	MUC.CL-1 [Trypanosoma cruzi]	59	45
746	1	3	554	gi|141858	replication-associated protein [Plasmid pAD1]	59	36
869	1	2	250	gi|1432153	cellobiose-specific PTS permease [Klebsiella oxytoca]	59	40
4	8	6948	6067	gi|147516	ribokinase [Escherichia coli]	58	42
11	6	3312	4121	gi|1732200	PTS permease for mannose subunit IIPMan [Vibrio furnissii]	58	35
16	9	7684	6932	gnl|PID|e233879	hypothetical protein [Bacillus subtilis]	58	48
23	14	7440	8903	gi|142940	ftsA [Bacillus subtilis]	58	39
30	2	570	1283	gi|1644202	unknown [Bacillus subtilis]	58	37
48	7	7186	8037	gi|1573247	hypothetical [Haemophilus influenzae]	58	35
49	7	2395	2871	gnl|PID|e210884	c2 gene product [Bacteriophage B1]	58	34
54	1	1014	91	gi|46645	ORF (rlx) [Staphylococcus aureus]	58	46
55	3	1221	511	gi|726443	No definition line found [Caenorhabditis elegans]	58	41
58	1	1904	696	gi|1591564	molybdenum cofactor biosynthesis moeA protein [Methanococcus jannaschii]	58	39
58	8	7238	6996	gi|1279769	FdhC [Methanobacterium thermoformicicum]	58	54
72	12	12117	10897	gi|763052	integrase [Bacteriophage T270]	58	37
77	2	1155	1910	gi|1245464	YfeA [Yersinia pestis]	58	34
78	1	2589	49	gi|40663	sialidase [Clostridium septicum]	58	40
88	9	5854	6528	gi|1619623	hemin binding protein [Yersinia enterocolitica]	58	37
93	6	2639	2863	gi|405133	putative [Bacillus subtilis]	58	33
98	13	13523	12432	gi|147329	transport protein [Escherichia coli]	58	41
100	12	8550	8224	gi|1736642	Invasin. [Escherichia coli]	58	47

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

C ntig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
102	7	5688	5969	gi|808869	human gcp372 [Homo sapiens]	58	30
105	5	3716	4501	gi|143729	transcription activator [Bacillus subtilis]	58	40
107	1	511	2	gi|1303827	YqfI [Bacillus subtilis]	58	34
108	2	1040	1732	gi|1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	58	37
114	6	7608	8444	gi|152719	flavocytochrome c [Shewanella putrefaciens]	58	40
117	14	11813	11115	gi|1575577	DNA-binding response regulator [Thermotoga maritima]	58	42
122	1	1	936	gi|393269	adhesion protein [Streptococcus pneumoniae]	58	38
123	23	20379	21617	gi|1653948	hypothetical protein [Synechocystis sp.]	58	38
133	8	7362	8480	gi|143498	degS protein [Bacillus subtilis]	58	38
133	9	8437	9087	gi|143089	iep protein [Bacillus subtilis]	58	31
138	3	3551	2898	gi|216114	DNA polymerase [Bacteriophage SPO1]	58	41
138	5	5819	5049	gnl|PID|e289148	highly similar to phosphotransferase system regulator [Bacillus subtilis]	58	38
138	17	11419	10379	gi|1674137	(AE000044) Mycoplasma pneumoniae, lipoate protein ligase; similar to Swiss-Prot Accession Number P32099, from E. coli [Mycoplasma pneumoniae]	58	37
139	8	5002	4808	gi|153607	dpnD gene product [Streptococcus pneumoniae]	58	43
146	9	7817	6627	gi|606076	ORF_o384 [Escherichia coli]	58	43
150	10	7529	7894	gi|141852	sialidase [Actinomyces viscosus]	58	28
152	10	5717	6637	gi|296356	putative membrane transport protein [Clostridium perfringens] pir|A56641|A56641 probable membrane transport protein - Clostridium perfringens	58	36
162	10	11009	11185	gi|42655	pi protein [Escherichia coli]	58	37
164	3	1793	1608	gi|881499	parathion hydrolase (phosphotriesterase)-	58	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					related protein [Mus usculus]		
165	6	5640	4975	gi|1146190	2-keto-3-deoxy-6-phosphogluconate aldolase [Bacillus subtilis]	58	39
165	10	9038	8199	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli]	58	35
168	1	1	657	gi|413930	ipa-6d gene product [Bacillus subtilis]	58	41
170	1	923	234	gi|1573505	hypothetical [Haemophilus influenzae]	58	30
176	1	1	1101	gi|1652379	cation-transporting P-ATPase [Synechocystis sp.]	58	30
180	12	10237	10410	gi|408123	V-ATPase 14kD subunit peptide [Drosophila melanogaster] pir|S38436|S38436 H+-transporting ATPase (EC 3.6.1.35) 14K chain - ruit fly (Drosophila melanogaster)	58	33
193	3	2077	1388	gi|1256633	putative [Bacillus subtilis]	58	39
193	4	2602	2075	gi|147920	3-methyladenine-DNA glycosylase I (tag) [Escherichia coli]	58	33
194	9	6492	5500	sp|P09997|YIDA_ECOLI	HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION.	58	38
201	5	5152	4466	gi|755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	58	28
210	9	6546	7265	gi|466520	pocR [Salmonella typhimurium]	58	36
220	1	3	569	gi|467441	expressed at the end of exponential growyh under condtions in which he enzymes of the TCA cycle are repressed [Bacillus subtilis] sp|P14194|CTC_BACSU GENERAL STRESS PROTEIN CTC. (SUB 2-204) gi|40219 partial ctc gene product (AA 1-186) [Bacillus subtilis]	58	38
222	10	6520	7143	gi|1674024	(AE000033) Mycoplasma pneumoniae,	58	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					hypothetical protein (yjfS) homolog; similar to Swiss-Prot Accession Number P39301, from E. coli [Mycoplasma pneumoniae]		
233	7	4984	3944	gi|147806	selenium metabolism protein [Escherichia coli]	58	45
238	14	12128	12910	gi|1736468	Pectin degradation repressor protein KdgR. [Escherichia coli]	58	37
244	11	8102	7809	gi|467418	unknown [Bacillus subtilis]	58	37
246	1	1	276	gi|65291	receptor tyrosine kiase preprotein [Xiphophorus sp.] ir|S06142|S06142 kinase-related transforming protein (Tu) (EC 7.1.-) precursor - southern platyfish	58	32
255	4	2927	2559	gi|1652384	ABC transporter [Synechocystis sp.]	58	41
258	9	8025	8966	gi|147402	mannose permease subunit III-Man [Escherichia coli]	58	35
259	2	1801	893	gi|1591564	molybdenum cofactor biosynthesis moeA protein [Methanococcus jannaschii]	58	39
260	3	1754	2254	gi|580841	F1 [Bacillus subtilis]	58	38
271	4	2382	2738	gi|40067	X gene product [Bacillus sphaericus]	58	37
279	8	6237	6536	gi|1783243	homologous to jojC gene product (B. subtilis; prf:2111327a); hypothetical [Bacillus subtilis]	58	34
301	1	753	175	gi|499196	ORF1 [Streptomyces lincolnensis]	58	37
304	1	100	849	gi|1653322	hypothetical protein [Synechocystis sp.]	58	41
313	2	748	1650	gi|1658371	cyclic beta-1,2-glucan modification protein [Rhizobium meliloti]	58	36
321	11	6033	6533	gi|1573292	hypothetical [Haemophilus influenzae]	58	34
322	6	3819	5069	gi|23897	5'-nucleotidase [Homo sapiens]	58	34
324	5	3259	4452	gi|1469784	putative cell division protein ftsW [Enterococcus hirae]	58	37
328	1	1	270	gi|882579	CG Site No. 29739 [Escherichia coli]	58	43

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
330	8	6228	6758	gi|43941	EIII-B Sor PTS [Klebsiella pneumoniae]	58	37
334	4	3634	3963	gi|1001306	hypothetical protein [Synechocystis sp.]	58	34
345	17	18899	20044	gi|853809	ORF3 [Clostridium perfringens]	58	30
363	7	8475	9944	gi|348056	trans-acting positive regulator [Bacillus anthracis]	58	33
375	7	6472	5279	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	58	42
394	12	10689	12095	gi|537034	ORF_o488 [Escherichia coli]	58	32
399	3	1383	2198	gi|580905	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis] gi|580919 Jag [Bacillus subtilis]	58	36
399	16	11544	12098	gi|1572965	hypothetical [Haemophilus influenzae]	58	39
399	19	14776	15654	gi|1778530	CitG homolog [Escherichia coli]	58	40
407	2	738	553	gi|170553	pyruvate kinase [Trichoderma reesei]	58	38
416	5	4045	3389	gi|475112	enzyme IIabc [Pediococcus pentosaceus]	58	41
449	4	1421	879	gi|928834	integrase [Lactococcus lactis phage BK5-T]	58	32
497	1	3	458	gi|160628	reticulocyte binding protein 2 [Plasmodium vivax]	58	30
594	1	285	4	gi|1353874	unknown [Rhodobacter capsulatus]	58	39
637	6	3451	2765	pir|D61615|D61615	sericin MG-1 - greater wax moth (fragment)	58	52
653	1	595	245	gi|1408585	LtrD [Lactococcus lactis lactis]	58	41
656	4	3713	5209	sp|P13692|P54_ENTFC	P54 PROTEIN PRECURSOR.	58	37
656	6	5988	6467	gi|1017818	phosphotyrosine protein phosphatase [Streptomyces coelicolor]	58	48
667	1	88	1467	bbs|177441	OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa]	58	40
686	1	892	233	pir|A24255|A24255	chorion class A protein L11 precursor -	58	38

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					silkworm		
706	1	1002	607	gi|1001762	hypothetical protein [Synechocystis sp.]	58	32
801	1	254	12	gnl|PID|e243641	unknown [Mycobacterium tuberculosis]	58	29
848	1	212	3	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	58	37
975	1	3	422	gi|290545	f270 [Escherichia coli]	58	35
11	4	2345	2833	gi|1439527	EIIA-man [Lactobacillus curvatus]	57	46
16	2	1426	365	gi|780550	acetyl transferase [Rhizobium loti]	57	35
18	3	1593	925	gnl|PID|e137594	xerC recombinase [Lactobacillus leichmannii]	57	36
19	15	8058	8267	gi|1590922	cell division inhibitor [Methanococcus jannaschii]	57	42
19	23	11938	12318	gi|1294760	structural protein; orfL3; putative [Bacteriophage phi-41]	57	46
25	9	7743	6958	gnl|PID|e255000	hypothetical protein [Bacillus subtilis]	57	40
47	3	3857	4462	gi|1353540	ORF23 [Bacteriophage r1t]	57	35
65	10	7180	8919	gi|496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	57	40
68	7	3923	3705	gi|336656	ribosomal protein secY [Cyanophora paradoxa]	57	28
70	4	2317	3645	pir|S11158|YESAEE	erythromycin resistance protein - Staphylococcus epidermidis plasmid pUL5050	57	40
76	1	55	1095	gi|1353562	Structural protein [Bacteriophage r1t]	57	41
91	11	9070	8849	gi|550321	beta-fructofuranosidase [Chenopodium rubrum]	57	30
94	4	1740	1495	gi|47406	penicillin-binding protein 1a [Streptococcus pneumoniae] ir|S28031|S28031 penicillin-binding protein 1a - Streptococcus eumoniae (strain 456) (fragment)	57	30
98	6	7766	6849	gi|409286	bmrU [Bacillus subtilis]	57	31

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
100	22	17294	15912	gnl|PID|e289150	member of the SNF2 helicase family [Bacillus subtilis]	57	30
102	1	66	2465	gi|405564	traE [Plasmid pSK41]	57	28
110	14	11757	12497	gi|854601	unknown [Schizosaccharomyces pombe]	57	38
114	9	10291	11139	gi|853777	product similar to E.coli PRFA2 protein [Bacillus subtilis] pir|S55438|S55438 ywkE protein - Bacillus subtilis sp|P45873|HEMK_BACSU POSSIBLE PROTOPORPHYRINOGEN OXIDASE (EC .3.3.-).	57	38
115	3	955	1461	gi|396347	alternate name yjaB [Escherichia coli]	57	33
123	3	1925	2932	gi|1001731	low affinity sulfate transporter [Synechocystis sp.]	57	39
124	7	6026	5118	gi|1674310	(AE000058) Mycoplasma pneumoniae, MG085 homolog, from M. genitalium [Mycoplasma pneumoniae]	57	30
128	9	7530	6235	gi|413940	ipa-16d gene product [Bacillus subtilis]	57	36
128	31	25487	25206	gi|1651915	hypothetical protein [Synechocystis sp.]	57	42
128	33	26878	26150	gi|1001387	hypothetical protein [Synechocystis sp.]	57	30
128	37	30730	29600	gi|406877	DivIB protein [Bacillus licheniformis]	57	35
130	9	7408	8556	gi|343539	NADH dehydrogenase subunit 4 [Trypanosoma brucei]	57	27
144	1	1013	219	gi|1652518	hypothetical protein [Synechocystis sp.]	57	45
144	6	4145	5254	gi|149581	maturation protein [Lactobacillus paracasei]	57	38
146	1	617	192	gi|147402	mannose permease subunit III-Man [Escherichia coli]	57	33
153	1	83	991	gi|147336	transmembrane protein [Escherichia coli]	57	33
160	8	4718	4134	gi|305333	zeta-crystallin [Cavia porcellus]	57	39
167	8	14891	14688	gi|206354	protein kinase C, zeta subspecies [Rattus norvegicus] pir|A30314|A30314 protein kinase C (EC 2.7.1.-) zeta - rat sp|P09217|KPCZ_RAT PROTEIN KINASE C, ZETA	57	39

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					TYPE (EC 2.7.1.-) NPKC-ZETA).		
174	1	760	2	gnl|PID|e191403	ORFA gene product [Chloroflexus aurantiacus]	57	42
176	4	3347	3568	gi|1236529	cyclomaltodextrinase [Bacillus sp.]	57	46
194	8	4786	5457	gi|405516	This ORF is homologous to nitroreductase from Enterobacter cloacae, ccession Number A38686, and Salmonella, Accession Number P15888 Mycoplasma-like organism]	57	26
199	3	3207	3764	gi|216350	ORF [Bacillus subtilis]	57	38
202	5	3356	3664	gi|1183841	Holliday junction binding protein [Pseudomonas aeruginosa]	57	34
202	12	10911	10192	gi|971338	anaerobic regulatory protein [Bacillus subtilis]	57	27
205	3	1022	468	gi|1783240	hypothetical [Bacillus subtilis]	57	38
223	2	779	1501	gi|1208965	hypothetical 23.3 kd protein [Escherichia coli]	57	32
223	3	1499	2332	gi|303560	ORF271 [Escherichia coli]	57	35
223	11	8404	12198	gi|158079	period protein [Drosophila serrata]	57	40
237	9	3685	3906	gi|514919	phosphofructokinase [Drosophila melanogaster]	57	31
242	7	5760	5020	gi|1574596	H. influenzae predicted coding region HI1738 [Haemophilus influenzae]	57	33
250	2	1243	1485	gnl|PID|e275819	K08G2.8 [Caenorhabditis elegans]	57	47
276	28	16565	16332	gi|886375	variant-specific surface protein [Plasmodium falciparum]	57	47
288	6	3157	3363	gi|147403	mannose permease subunit II-P-Man [Escherichia coli]	57	39
289	1	141	818	gi|1742822	Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli]	57	40
292	20	15930	15721	gi|854201	putative polymerase [Infectious bursal disease virus]	57	47
294	4	1454	2014	gi|454303	LDJ2 gene product [Allium porrum]	57	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
295	4	2052	2342	pir|S48588|S48588	hypothetical protein - Mycoplasma capricolum (SGC3) (fragment)	57	39
301	14	10921	10148	gnl|PID|e262045	putative orf [Bacillus subtilis]	57	38
306	1	2	793	gi|216715	HpaI methyltransferase [Haemophilus parainfluenzae] pir|S28681|S28681 site-specific DNA-methyltransferase adenine-specific) (EC 2.1.1.72) HpaI - Haemophilus parainfluenzae sp|P29538|MTH1_HAEPA MODIFICATION METHYLASE HPAI (EC 2.1.1.72) ADENINE-SPECIFIC MET	57	36
306	8	5418	5663	gi|1591542	M. jannaschii predicted coding region MJ0857 [Methanococcus jannaschii]	57	42
308	2	1732	1487	gi|1518045	FlbF protein [Borrelia burgdorferi]	57	28
321	2	1030	1458	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli]	57	30
351	4	2342	1587	gi|1591853	M. jannaschii predicted coding region MJ1222 [Methanococcus jannaschii]	57	37
355	30	20619	20861	gi|1136394	There are three putative hydrophobic domains in the central region. [Homo sapiens]	57	42
364	10	9415	8852	gi|38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir|A29277|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus	57	32
365	3	4715	1812	gi|914990	Similar to DEAD box family helicases [Saccharomyces cerevisiae] pir|S59797|S59797 hypothetical protein D9798.1 - yeast Saccharomyces cerevisiae)	57	35
378	1	615	10	gi|1652989	hypothetical protein [Synechocystis sp.]	57	35
379	1	1457	114	gi|1256618	transport protein [Bacillus subtilis]	57	36
390	1	1426	2	gi|387880	collagen adhesin [Staphylococcus aureus]	57	37

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
422	1	2	409	gi|1591837	M. jannaschii predicted coding region MJ1207 [Methanococcus jannaschii]	57	37
447	1	397	131	gi|214566	keratin protein XK81 [Xenopus laevis]	57	33
454	2	1095	889	gi|1783256	sigma factor [Bacillus subtilis]	57	28
504	2	641	1426	gi|42081	nagD gene product (AA 1-250) [Escherichia coli]	57	32
524	2	963	577	gi|143724	putative [Bacillus subtilis]	57	43
535	4	4862	4305	gi|146549	kdpC [Escherichia coli]	57	40
547	2	426	719	gi|533098	DnaD protein [Bacillus subtilis]	57	33
548	1	316	717	gi|397973	Mg2+ transport ATPase [Salmonella typhimurium]	57	33
639	2	359	105	gnl|PID|e247390	P-type ATPase [Dictyostelium discoideum]	57	31
641	1	941	180	gnl|PID|e261990	putative orf [Bacillus subtilis]	57	36
686	3	1298	3259	gi|496506	orf gamma [Streptococcus pyogenes]	57	37
686	6	2200	2847	gi|404800	putative [Saccharopolyspora erythraea]	57	47
782	2	591	860	gi|1591270	alanyl-tRNA synthetase [Methanococcus jannaschii]	57	32
844	1	3	182	gi|849217	Weak similarity to Streptococcus Protein V, a type-II IgG receptor PIR accession number S17354) and Giardia lamblia median body rotein (PIR accession number S33821) [Saccharomyces cerevisiae] pir|S61181|S61181 hypothetical protein D9740.10 - yeast Sacchar	57	34
859	1	174	4	gi|1762584	polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana]	57	28
967	1	381	4	gi|309662	pheromone binding protein [Plasmid pCF10]	57	40
11	5	2817	3314	gi|43941	EIII-B Sor PTS [Klebsiella pneumoniae]	56	30
15	1	80	892	gi|1574803	spermidine/putrescine-binding periplasmic protein precursor (potD) [Haemophilus influenzae]	56	32
37	8	6327	6088	gi|290561	o188 [Escherichia coli]	56	41

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
44	2	1169	1360	gi|16096	peroxidase [Armoracia rusticana]	56	37
56	3	1881	1363	gi|49272	Asparaginase [Bacillus licheniformis]	56	33
65	1	102	887	gi|1377832	unknown [Bacillus subtilis]	56	41
75	9	5817	4306	gi|1235712	polyprotein [Infectious pancreatic necrosis virus]	56	30
83	7	3260	4051	gi|1652645	phosphoglycolate phosphatase [Synechocystis sp.]	56	30
95	3	1793	2389	pir|C53610|C53610	ntpE protein - Enterococcus hirae	56	28
100	3	5076	1915	gi|1353559	ORF42 [Bacteriophage r1t]	56	35
100	16	10581	10369	gi|868224	No definition line found [Caenorhabditis elegans]	56	35
100	48	31841	32770	gi|460025	ORF2, putative [Streptococcus pneumoniae]	56	38
108	5	4007	3336	gi|288301	ORF2 gene product [Bacillus megaterium]	56	34
109	2	1032	325	gi|413976	ipa-52r gene product [Bacillus subtilis]	56	36
119	7	3958	5304	gi|498842	VirS [Clostridium perfringens]	56	35
123	32	29479	30345	gi|39981	P30 [Bacillus subtilis]	56	38
126	1	521	3	gi|147403	mannose permease subunit II-P-Man [Escherichia coli]	56	29
130	6	4296	6104	gi|308854	oligopeptide binding protein [Lactococcus lactis]	56	33
131	7	5267	6613	gi|466589	CG Site No. 39 [Escherichia coli]	56	32
133	5	4358	5758	gi|1573431	aminodeoxychorismate lyase (pabC) [Haemophilus influenzae]	56	40
138	20	13680	12670	gi|1590951	UDP-glucose 4-epimerase [Methanococcus jannaschii]	56	40
138	29	19764	18823	gi|44864	H.8 outer membrane protein (AA -17 to 71) [Neisseria gonorrhoeae] ir|S02720|S02720 outer membrane protein H.8 precursor - Neisseria norrhoeae	56	33
145	7	5611	7179	gi|1652892	ABC transporter [Synechocystis sp.]	56	33
146	10	8545	7811	gi|41519	P30 protein (AA 1-240) [Escherichia coli]	56	28

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
150	4	2979	4637	gi|309662	pheromone binding protein [Plasmid pCF10]	56	32
159	5	5362	5066	gi|576733	apocytochrome b [Trypanoplasma borreli]	56	43
164	13	8864	15031	gi|1654116	protein F2 [Streptococcus pyogenes]	56	43
179	7	7790	9118	gi|413926	ipa-2r gene product [Bacillus subtilis]	56	33
187	4	2239	1667	gi|1573061	hypothetical [Haemophilus influenzae]	56	18
200	19	11473	10724	gi|498817	ORF8; homologous to small subunit of phage terminases [Bacillus ubtilis]	56	35
206	6	3766	2759	gi|474837	ORF1 [Thermoanaerobacterium thermosulfurigenes] sp|P38541|YAMB_THETU HYPOTHETICAL 35.6 KD PROTEIN IN AMYB 5'REGION ORF1).	56	34
207	2	2091	1672	gi|1204258	soluble protein [Escherichia coli]	56	40
217	9	6661	6158	gi|1017427	elastic titin [Homo sapiens]	56	28
225	7	6007	5099	gi|1742675	Phosphotransferase system enzyme II (EC 2.7.1.69) MalX [Escherichia coli]	56	46
230	3	595	3153	gi|437706	alternative truncated translation product from E.coli [Streptococcus neumoniae]	56	34
236	2	1486	515	gi|415664	catabolite control protein [Bacillus megaterium] sp|P46828|CCPA_BACME GLUCOSE-RESISTANCE AMYLASE REGULATOR CATABOLITE CONTROL PROTEIN).	56	35
236	7	9255	8599	gi|343544	ATPase 6 [Trypanosoma brucei]	56	48
238	15	13059	13718	gi|1146190	2-keto-3-deoxy-6-phosphogluconate aldolase [Bacillus subtilis]	56	37
238	20	17734	18756	gi|1574060	hypothetical [Haemophilus influenzae]	56	32
238	23	21613	20726	gi|151361	member of the AraC/XylS family of transcriptional regulators Pseudomonas aeruginosa]	56	36
242	6	4103	4477	gi|886858	nicotinic acetylcholine receptor [Caenorhabditis elegans] pir|S57648|S57648 nicotinic acetylcholine receptor - Caenorhabditis legans	56	35

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
260	5	3170	3781	gnl|PID|e58151	F3 [Bacillus subtilis]	56	43
279	6	5140	2831	gi|581100	gamma-glutamylcysteine synthetase (aa 1-518) [Escherichia coli] pir|A24136|SYECEC glutamate--cysteine ligase (EC 6.3.2.2) - scherichia coli	56	42
279	9	6434	7228	gi|1783243	homologous to jojC gene product (B. subtilis; prf:2111327a); hypothetical [Bacillus subtilis]	56	29
292	14	10719	11504	gi|45738	ORFC [Enterococcus faecalis]	56	37
313	3	3039	1831	gi|474915	orf 337; translated orf similarity to SW: BCR_ECOLI bicyclomycin esistance protein of Escherichia coli [Coxiella burnetii] pir|S44207|S44207 hypothetical protein 337 - Coxiella burnetii (SUB -338)	56	31
313	5	4233	3589	gi|405883	yeiL [Escherichia coli]	56	30
322	5	1994	3715	gi|1377831	unknown [Bacillus subtilis]	56	34
353	2	2353	1310	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	56	26
394	14	13289	14143	gi|142836	repressor protein [Bacillus subtilis]	56	30
399	32	30208	30891	gi|396293	similar to Bacillus subtilis hypoth. 20 kDa protein, in tsr 3' egion [Escherichia coli]	56	38
402	2	1267	914	gi|170710	alpha-type gliadin precursor protein [Triticum aestivum]	56	45
408	4	2825	2220	gnl|PID|e257696	collagen binding protein [Lactobacillus reuteri]	56	36
432	5	3105	3302	gi|11678	atpE gene product [Marchantia polymorpha]	56	33
443	2	844	1089	gi|1256138	YbbI [Bacillus subtilis]	56	36
499	2	875	1666	gi|1499876	magnesium and cobalt transport protein [Methanococcus jannaschii]	56	30
510	6	3864	4733	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	56	34

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
543	6	3706	3113	gi|563812	XCAP-C [Xenopus laevis]	56	32
609	2	390	653	gi|48745	principal sigma subunit (AA 1-442) [Streptomyces coelicolor] ir|S11712|S11712 translation initiation factor sigma hrdB - reptomyces coelicolor	56	37
626	2	1124	2104	gi|950197	unknown [Corynebacterium glutamicum]	56	40
787	1	2	634	gnl|PID|e283826	orf c04012 [Sulfolobus solfataricus]	56	26
820	1	1220	3	gi|44001	galactose-1-P-uridyl transferase [Lactobacillus helveticus] ir|B47032|B47032 galactose-1-phosphate uridyl transferase - ctobacillus helveticus	56	35
875	1	1	144	gi|455178	16K protein [Escherichia coli]	56	46
906	2	307	846	gi|144858	ORF A [Clostridium perfringens]	56	34
941	1	3	335	gi|160299	glutamic acid-rich protein [Plasmodium falciparum] pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum	56	23
5	5	2451	2951	gi|1303811	YqeU [Bacillus subtilis]	55	39
8	10	8312	7947	gi|1196907	daunorubicin resistance protein [Streptomyces peucetius]	55	29
17	24	23626	24465	gnl|PID|e285322	RecX protein [Mycobacterium smegmatis]	55	28
17	31	31027	30344	gi|143830	xpaC [Bacillus subtilis]	55	22
17	34	31991	32302	gnl|PID|e229183	C11G6.3 [Caenorhabditis elegans]	55	34
30	1	2	478	pir|S10655|S10655	hypothetical protein X - Pyrococcus woesei (fragment)	55	34
49	14	9998	10411	gi|455154	ORF D [Clostridium perfringens]	55	36
54	3	955	1332	gnl|PID|e238660	hypothetical protein [Bacillus subtilis]	55	32
54	10	3527	3231	pir|JQ0405|JQ0405	hypothetical 119.5K protein (uvrA region) - Micrococcus luteus	55	45
67	4	2313	3044	gi|555750	unknown [Neisseria gonorrhoeae]	55	42
69	4	2250	2020	gnl|PID|e259955	K04G11.5 [Caenorhabditis elegans]	55	33

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
77	5	3954	2938	gi|1001634	hypothetical protein [Synechocystis sp.]	55	34
80	4	4806	2482	gi|466952	B1620_F1_30 [Mycobacterium leprae]	55	35
81	6	4212	3730	gi|606073	ORF_o169 [Escherichia coli]	55	34
83	1	66	737	gi|216064	morphogenesis protein B [Bacteriophage PZA]	55	36
89	10	9486	7714	gi|148221	DNA-dependent ATPase, DNA helicase [Escherichia coli] pir|JS0137|BVECRQ recQ protein - Escherichia coli	55	35
91	5	2507	3289	gi|153015	FemA protein [Staphylococcus aureus]	55	35
100	14	9974	9393	gi|558603	synaptonemal complex protein 1 [Mus musculus]	55	30
116	1	1	909	gi|473901	ORF1 [Lactococcus lactis]	55	33
122	3	1801	2655	gi|1016216	putative protein of 299 amino acids [Cyanophora paradoxa]	55	28
123	30	28191	28721	gi|1142714	phosphoenolpyruvate:mannose phosphotransferase element IIB [Lactobacillus curvatus]	55	29
128	22	16664	16029	gi|606025	ORF_o221 [Escherichia coli]	55	42
150	7	5949	6521	gi|39573	P20 (AA 1-178) [Bacillus licheniformis]	55	32
155	7	5767	6660	gi|1763974	DPPA [Bacillus methanolicus]	55	31
157	1	867	70	gi|1067010	M153.1 [Caenorhabditis elegans]	55	34
160	9	6090	4804	gi|1592141	M. jannaschii predicted coding region MJ1507 [Methanococcus jannaschii]	55	31
176	3	2060	3349	gi|153858	wall-associated protein [Streptococcus mutans]	55	37
201	2	3277	413	gi|1235662	RfbC [Myxococcus xanthus]	55	36
202	9	6199	8001	gi|606018	ORF_o783 [Escherichia coli]	55	42
222	7	4803	4021	gnl|PID|e289148	highly similar to phosphotransferase system regulator [Bacillus subtilis]	55	40
238	12	11465	9942	gnl|PID|e266573	unknown [Mycobacterium tuberculosis]	55	27
238	13	11527	12027	gi|1129093	unknown protein [Bacillus sp.]	55	36

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
240	4	1988	1215	gnl|PID|e252616	DcuC protein [Escherichia coli]	55	34
246	2	433	792	gnl|PID|e233868	hypothetical protein [Bacillus subtilis]	55	25
253	5	1827	1549	gi|142540	aspartokinase II [Bacillus sp.]	55	48
259	1	895	74	gi|1006621	molybdate-binding periplasmic protein [Synechocystis sp.]	55	37
267	1	1183	2	gi|882672	ORF_o313 [Escherichia coli]	55	27
292	16	12843	13325	gi|561746	cyclin-dependent protein kinase [Mus musculus]	55	26
294	9	3390	3752	gi|984582	DinJ [Escherichia coli]	55	26
300	5	3914	3582	gi|1591957	M. jannaschii predicted coding region MJ1318 [Methanococcus jannaschii]	55	38
305	3	2769	3527	gi|606309	ORF_o265; gtg start [Escherichia coli]	55	36
320	6	4479	3475	gi|1591732	cobalt transport ATP-binding protein O [Methanococcus jannaschii]	55	32
355	24	18149	18322	gi|344751	MDV TK gene product [unidentified]	55	40
364	2	2083	386	gi|1573045	hypothetical [Haemophilus influenzae]	55	40
364	9	8796	8575	gnl|PID|e252108	ORF YOR255w [Saccharomyces cerevisiae]	55	27
379	8	8248	6872	gi|1330236	dihydropyrimidinase [Homo sapiens]	55	37
386	6	3847	4332	gi|976025	HrsA [Escherichia coli]	55	27
441	2	939	1730	gi|144859	ORF B [Clostridium perfringens]	55	28
482	6	3515	3156	gi|606162	ORF_f229 [Escherichia coli]	55	39
497	9	4885	5937	gi|1041637	replication initiator protein [Staphylococcus xylosus]	55	33
546	1	1	1104	gi|467446	similar to SpoVB [Bacillus subtilis]	55	36
634	4	2132	1524	gi|431950	similar to a B.subtilis gene (GB: BACHEMEHY_5) [Clostridium asteurianum]	55	27
660	2	249	401	gnl|PID|e254995	hypothetical protein [Bacillus subtilis]	55	35
671	1	288	58	gi|38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir|A29277|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus	55	33

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
686	2	245	1141	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	55	36
713	3	2742	1438	gnl|PID|e8901	RESA NF7 Ag13 [Plasmodium falciparum]	55	25
815	1	2	226	gi|1113815	histidine kinase [Borrelia burgdorferi]	55	36
857	1	2	520	gi|143024	glucose-resistance amylase regulator [Bacillus subtilis] pir|S15318|S15318 ccpA protein - Bacillus subtilis sp|P25144|CCPA_BACSU GLUCOSE-RESISTANCE AMYLASE REGULATOR CATABOLITE CONTROL PROTEIN).	55	31
931	1	3	557	gi|1098508	putative spore germination apparatus protein [Bacillus megaterium]	55	32
17	7	6379	7218	gnl|PID|e250887	potential coding region [Clostridium difficile]	54	35
21	9	7265	6348	gi|13441	NADH dehydrogenase subunit 4L [Phoca vitulina]	54	29
28	2	2727	3425	gi|1001792	hypothetical protein [Synechocystis sp.]	54	29
32	6	4044	3523	gi|1673660	(AE000002) Mycoplasma pneumoniae, hypothetical 28K protein; similar to GenBank Accession Number JS0068, from M. pneumoniae [Mycoplasma pneumoniae]	54	36
33	3	2274	3767	gnl|PID|e245024	unknown [Mycobacterium tuberculosis]	54	36
40	1	1	915	gi|773349	BirA protein [Bacillus subtilis]	54	32
49	6	2120	2485	gnl|PID|e139446	a2 gene product [Bacteriophage B1]	54	38
54	17	8969	8661	gi|334068	ORF2 [Suid herpesvirus 1]	54	51
65	2	1311	2120	gi|537207	ORF_f277 [Escherichia coli]	54	27
72	20	21986	22435	gi|928848	ORF70'; putative [Lactococcus lactis phage BK5-T]	54	34
105	4	3039	3827	gnl|PID|e205174	orf2 gene product [Lactobacillus helveticus]	54	30
127	1	884	150	gi|726443	No definition line found [Caenorhabditis	54	31

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					elegans]		
148	1	1204	62	gi|467456	unknown [Bacillus subtilis]	54	37
156	4	4360	3167	gi|1032483	unidentified ORF downstream of hydrogenase cluster; ORF5 [Anabaena variabilis]	54	30
160	4	1523	2077	gnl|PID|e255111	hypothetical protein [Bacillus subtilis]	54	27
160	7	4260	3745	gi|1184121	auxin-induced protein [Vigna radiata]	54	30
165	5	4996	3971	gi|1772652	2-keto-3-deoxygluconate kinase [Haloferax alicantei]	54	36
176	2	1044	1937	gi|162201	P-type ATPase [Trypanosoma brucei]	54	38
180	29	30833	29853	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	54	29
200	16	7933	6656	gi|1574238	traN protein (traN) [Haemophilus influenzae]	54	31
206	1	232	2	gi|1220501	Rickettsia tsutsugamushi (strain Kp47) gene, complete cds [Rickettsia tsutsugamushi]	54	31
220	4	5235	4342	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli]	54	31
220	5	5821	5135	gi|43942	first subunit of EII-Sor [Klebsiella pneumoniae]	54	36
223	20	17253	17747	gi|47932	tonB protein [Salmonella typhimurium]	54	38
228	7	4866	4033	gi|1736828	Thi4 protein [Escherichia coli]	54	34
229	4	5050	3371	gi|1046078	M. genitalium predicted coding region MG369 [Mycoplasma genitalium]	54	42
236	3	4777	1496	gi|152271	319-kDA protein [Rhizobium meliloti]	54	28
236	5	7822	6944	gnl|PID|e285031	Hyp1 protein [Hydra vulgaris]	54	20
238	30	27964	27746	gnl|PID|e217586	PlnM [Lactobacillus plantarum]	54	42
242	5	3508	4050	gi|149502	beta-lactamase [Lactococcus lactis]	54	35
257	1	296	120	gi|1498064	AtE1 [Arabidopsis thaliana]	54	50
257	6	6745	5633	gi|343949	var1(40.0) [Saccharomyces cerevisiae]	54	42

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
258	8	7839	7114	gi|41519	P30 protein (AA 1-240) [Escherichia coli]	54	31
276	20	13101	12880	gi|155322	icsB gene product [Plasmid pWR100]	54	37
280	1	618	106	gi|467356	unknown [Bacillus subtilis]	54	21
288	4	2183	2632	gi|39978	P16 [Bacillus subtilis]	54	39
316	1	3	767	gi|143264	membrane-associated protein [Bacillus subtilis]	54	34
318	7	5035	4565	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli]	54	28
319	3	1393	2163	gi|148327	vancomycin response regulator [Enterococcus faecium]	54	34
323	2	1256	2560	gi|413940	ipa-16d gene product [Bacillus subtilis]	54	26
364	7	7335	7724	gnl|PID|e250171	F18C12.1 [Caenorhabditis elegans]	54	31
386	5	2399	3844	gi|155369	PTS enzyme-II fructose [Xanthomonas campestris]	54	37
392	3	2004	3353	gi|872306	integral membrane protein [Streptomyces pristinaespiralis] pir|S57509|S57509 integral membrane protein - Streptomyces ristinaespiralis	54	32
424	5	1553	1371	gi|160316	major merozoite surface antigen [Plasmodium falciparum] sp|P50495|MSP1_PLAFP MEROZOITE SURFACE PROTEIN 1 PRECURSOR MEROZOITE SURFACE ANTIGENS) (PMMSA) (GP195).	54	37
445	2	1897	1178	gi|1781503	MigA [Pseudomonas aeruginosa]	54	31
452	5	2506	2805	gi|216292	neopullulanase [Bacillus sp.]	54	34
457	2	2178	1024	gi|405570	TraK protein shares sequence similarity with a family of proteins ncoded on Gram-negative gene transfer systems such as TraD from the plasmid [Plasmid pSK41]	54	35
461	3	627	1418	gi|797332	MocD [Agrobacterium tumefaciens]	54	38
466	5	5419	3770	gi|1652892	ABC transporter [Synechocystis sp.]	54	29

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
475	3	2745	1990	gi|532546	ORF13 [Enterococcus faecalis]	54	35
495	1	2	295	gi|304990	ORF_o290 [Escherichia coli]	54	21
502	4	3518	3216	gi|1573270	hemolysin (tlyC) [Haemophilus influenzae]	54	33
510	5	3089	3931	gi|1732200	PTS permease for mannose subunit IIPMan [Vibrio furnissii]	54	29
570	1	1	930	gi|1001582	penicillin-binding protein 1A [Synechocystis sp.]	54	31
573	6	2763	3164	gi|416197	homologous to plasmid R100 pemK gene [Escherichia coli]	54	35
590	1	433	2	gi|532309	25 kDa protein [Escherichia coli]	54	33
643	2	1202	1477	gnl|PID|e125689	256 kD golgin [Homo sapiens]	54	29
705	1	2	682	gi|148921	LicD protein [Haemophilus influenzae]	54	39
730	1	370	167	gnl|PID|e245531	ORF YLR068w [Saccharomyces cerevisiae]	54	29
745	1	502	209	gi|581140	NADH dehydrogenase [Escherichia coli]	54	37
749	1	413	3	gi|664840	TagB [Dictyostelium discoideum]	54	44
932	1	3	320	gi|537207	ORF_f277 [Escherichia coli]	54	27
4	6	5671	4748	gi|216267	ORF2 [Bacillus megaterium]	53	34
16	8	6231	6806	gi|517105	spermidine acetyltransferase [Escherichia coli]	53	35
17	1	2	2497	gi|387880	collagen adhesin [Staphylococcus aureus]	53	35
42	4	2942	3529	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	53	20
69	6	3149	4879	gi|1486244	unknown [Bacillus subtilis]	53	30
72	3	1455	2063	gi|1592197	M. jannaschii predicted coding region MJ1576 [Methanococcus jannaschii]	53	32
79	1	83	592	gi|633757	pr2 [Mycoplasma hyopneumoniae]	53	28
83	8	5179	4412	gi|496100	unknown function; putative [Bacteriophage phi-LC3]	53	39
85	10	7180	6764	gi|1303940	YqiU [Bacillus subtilis]	53	35
92	2	789	986	gi|1372996	Rho [Borrelia burgdorferi]	53	28

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
95	10	7546	7734	gi|162379	variant surface glycoprotein [Trypanosoma brucei]	53	28
99	4	1391	1861	gi|1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	53	34
100	44	29982	29749	gi|1590997	M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii]	53	35
102	5	4787	5089	gi|1399011	immunogenic secreted protein precursor [Streptococcus pyogenes]	53	40
113	1	825	4	gnl|PID|e264148	unknown [Mycobacterium tuberculosis]	53	24
114	4	6555	5113	gi|487282	Na+ -ATPase subunit J [Enterococcus hirae]	53	33
119	6	3581	3994	gi|473707	positive regulator for virulence factors [Clostridium perfringens]	53	31
123	19	16463	18115	gi|1591361	NADH oxidase [Methanococcus jannaschii]	53	33
136	1	381	4	gi|152744	IpaD protein [Shigella flexneri]	53	32
138	9	8079	7594	gi|467371	LACI family of transcriptional repreesor (probable) [Bacillus ubtilis]	53	29
142	8	4594	4007	gi|755216	N-acetylmuramidase [Lactococcus lactis]	53	38
162	12	12482	11937	gi|1063250	low homology to P20 protein of Bacillus lichiniformis and bleomycin acetyltransferase of Streptomyces verticillus [Bacillus subtilis]	53	36
163	1	546	31	gi|153767	ORF [Streptococcus pneumoniae]	53	34
163	7	4973	3453	gi|29468	beta-myosin heavy chain (1151 AA) [Homo sapiens]	53	36
167	2	1038	2006	gi|413930	ipa-6d gene product [Bacillus subtilis]	53	27
173	11	8865	7843	gi|1778569	YaaF homolog [Escherichia coli]	53	39
190	8	6842	3549	gi|387880	collagen adhesin [Staphylococcus aureus]	53	38
199	2	2725	950	gi|1652570	nitrate transport protein NrtB [Synechocystis sp.]	53	32
200	13	6184	5954	gi|1652679	hypothetical protein [Synechocystis sp.]	53	40
200	17	9287	7890	gi|1574246	H. influenzae predicted coding region	53	35

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					HI1409 [Haemophilus influenzae]		
205	6	2048	3229	gi|148026	topoisomerase III [Escherichia coli]	53	32
211	2	270	1052	gi|483940	transcription regulator [Bacillus subtilis]	53	30
221	10	5119	5994	gi|1353529	ORF12 [Bacteriophage r1t]	53	44
232	7	4344	3925	gi|1665759	Similar to Schistosoma mansoni amino acid permease (L25068). [Homo sapiens]	53	35
238	21	18705	19247	gi|1574062	hypothetical [Haemophilus influenzae]	53	30
239	1	2	1636	gi|433932	activator of (R)-hydroxyglutaryl-CoA dehydratase [Acidaminococcus ermentans]	53	35
250	1	1469	318	gi|987094	membrane transport protein [Streptomyces hygroscopicus]	53	22
253	4	1759	1028	gi|537245	aspartokinase I-homoserine dehydrogenase I [Escherichia coli] pir|S56629|S56629 aspartate kinase (EC 2.7.2.4) / homoserine ehydrogenase (EC 1.1.1.3) - Escherichia coli	53	35
271	8	4649	5800	gi|413966	ipa-42d gene product [Bacillus subtilis]	53	27
276	26	15786	15112	gi|1699017	ErpB2 [Borrelia burgdorferi]	53	26
279	11	8309	7797	gi|1651934	hypothetical protein [Synechocystis sp.]	53	35
288	8	3997	4872	gi|43943	second subunit of EII-Sor [Klebsiella pneumoniae]	53	32
290	6	4391	5680	gi|466882	pps1; B1496_C2_189 [Mycobacterium leprae]	53	29
294	3	1197	1481	gi|173004	topoisomerase I [Saccharomyces cerevisiae]	53	40
330	3	2351	3367	gi|466691	No definition line found [Escherichia coli]	53	34
334	8	8172	9182	gi|1652483	hypothetical protein [Synechocystis sp.]	53	29
368	1	620	102	gi|487273	Na+ -ATPase subunit I [Enterococcus hirae]	53	29
377	4	2424	2260	gi|221407	FP5 [Fowlpox virus]	53	35
382	1	257	36	gi|1592016	M. jannaschii predicted coding region MJ1371 [Methanococcus jannaschii]	53	32

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
387	1	2	460	gi|1574317	repressor protein (GP:L22692_1) [Haemophilus influenzae]	53	30
394	10	8379	10412	gi|882463	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia oli]	53	34
399	4	2349	3098	gi|453287	OmpR protein [Escherichia coli]	53	27
420	2	1378	719	gi|1437473	nitrate transporter [Bacillus subtilis]	53	28
441	6	5361	7937	gi|1592205	M. jannaschii predicted coding region MJ1595 [Methanococcus jannaschii]	53	38
461	1	6	512	gi|1651800	L-glutamine:D-fructose-6-P amidotransferase [Synechocystis sp.]	53	29
497	3	1700	1960	gi|4328	RIF1 gene product [Saccharomyces cerevisiae]	53	33
503	1	669	4	gnl|PID|e202290	unknown [Lactobacillus sake]	53	30
538	2	1053	262	gi|1613769	response regulator [Streptococcus pneumoniae]	53	30
539	6	6172	5183	gi|567887	putative repressor [Streptomyces peucetius]	53	32
551	1	629	162	gi|1256649	putative [Bacillus subtilis]	53	26
557	1	9	695	gi|143177	putative [Bacillus subtilis]	53	31
569	2	418	1158	gi|1184684	MucD [Pseudomonas aeruginosa]	53	26
614	1	99	581	gi|485280	28.2 kDa protein [Streptococcus pneumoniae]	53	32
660	1	1	279	gnl|PID|e288480	R10E8.f [Caenorhabditis elegans]	53	34
776	1	3	635	gi|151352	mandelate racemase (EC 5.1.2.2) [Pseudomonas putida]	53	33
11	2	1117	1656	gi|143150	levR [Bacillus subtilis]	52	29
17	6	5327	6559	gnl|PID|e250887	potential coding region [Clostridium difficile]	52	37
19	31	17760	17978	gi|1079556	dShc [Drosophila melanogaster]	52	42
19	38	20306	22627	gnl|PID|e139448	host interacting protein [Bacteriophage B1]	52	32

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
25	4	2662	2087	gi|1072067	PepF [Rhodobacter sphaeroides]	52	23
25	6	5596	3407	gi|1303866	YqgS [Bacillus subtilis]	52	34
49	3	1135	1569	gi|496279	putative [Bacteriophage Tuc2009]	52	25
53	1	850	2	sp|P52697|YBHE_ECOLI	HYPOTHETICAL 30.2 KD PROTEIN IN MODC 3'REGION.	52	35
54	9	10909	2687	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	52	30
57	6	4779	8402	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	52	31
58	6	6446	5949	gnl|PID|e255921	F53F4.10 [Caenorhabditis elegans]	52	31
72	13	13446	13195	gi|532541	ORF8 [Enterococcus faecalis]	52	37
81	17	13692	12520	gi|1732203	GlcNAc 6-P deacetylase [Vibrio furnissii]	52	35
84	1	3	1355	gi|64288	fast skeletal muscle Ca-ATPase [Rana esculenta]	52	34
100	2	1917	1027	gi|1353560	ORF43 [Bacteriophage r1t]	52	34
101	1	30	1862	gi|405957	yeeF [Escherichia coli]	52	24
106	8	8517	7600	gi|454904	rfbG gene product [Shigella flexneri]	52	41
108	1	1	1059	gnl|PID|e255337	unknown [Mycobacterium tuberculosis]	52	29
123	4	2899	3495	gi|1305720	prs-associated putative membrane protein [Escherichia coli]	52	24
128	23	17561	16740	gi|473805	'regulatory protein sfs1 involved in maltose metabolism' Escherichia coli]	52	32
130	8	6693	7481	gi|1552775	ATP-binding protein [Escherichia coli]	52	30
138	1	40	1359	gi|1045867	oligoendopeptidase F [Mycoplasma genitalium]	52	31
138	2	2757	1384	gi|1591425	hypothetical protein (GP:X91006_2) [Methanococcus jannaschii]	52	26
138	6	6317	5940	gi|1486247	unknown [Bacillus subtilis]	52	36
142	10	7337	5466	gi|1151158	repeat organellar protein [Plasmodium chabaudi]	52	34
149	1	33	1133	gi|1762962	FemA [Staphylococcus simulans]	52	31

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
161	1	3	245	gi|151276	histidine utilization genes repressor protein (hut) [Pseudomonas utida]	52	35
163	4	2048	1320	gi|1064810	function unknown [Bacillus subtilis]	52	27
164	8	4882	5103	gi|57251	precursor (AA -35 to 1766) [Rattus norvegicus]	52	38
165	9	7247	7474	gi|1652671	hypothetical protein [Synechocystis sp.]	52	28
178	5	1887	1681	gi|220704	cAMP-dependent protein kinase catalytic subunit-beta [Rattus sp.] gi|191177 cAMP-dependent protein kinase beta-catalytic subunit Cricetulus sp.]	52	36
180	24	22536	23774	gi|581052	cytosine deaminase [Escherichia coli]	52	28
190	9	8891	7056	gi|1592079	M. jannaschii predicted coding region MJ1429 [Methanococcus jannaschii]	52	39
195	8	2000	2272	gi|868024	HIC-1 gene product [Homo sapiens]	52	52
202	11	9189	10145	gi|141861	traA gene product [Plasmid pAD1]	52	33
204	4	1361	2011	gi|1184118	mevalonate kinase [Methanobacterium thermoautotrophicum]	52	33
204	8	4018	5142	gnl|PID|e283860	carotenoid biosynthetic gene ERWCRTS homolog [Sulfolobus solfataricus]	52	31
208	2	1112	2296	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	52	35
215	1	772	2	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	52	26
218	4	4072	3425	gi|862630	glyceraldehyde-3-phosphate dehydrogenase [Buchnera aphidicola] sp|Q07234|G3P_BUCAP GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC .2.1.12) (GAPDH).	52	35
228	1	1	741	gnl|PID|e264148	unknown [Mycobacterium tuberculosis]	52	29
230	2	149	634	gi|437705	hyaluronidase [Streptococcus pneumoniae]	52	28
233	8	6166	4982	gi|1001708	NifS [Synechocystis sp.]	52	31
240	3	725	967	gi|399655	Ca2+ regulatory protein [Saccharomyces	52	21

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					cerevisiae] sp|P35206|CSG2_YEAST CSG2 PROTEIN PRECURSOR.		
288	7	3171	4028	gi|147403	mannose permease subunit II-P-Man [Escherichia coli]	52	27
318	1	7	819	gi|1303849	YggB [Bacillus subtilis]	52	33
330	1	1062	154	gi|144859	ORF B [Clostridium perfringens]	52	29
330	9	6815	7213	gi|1439527	EIIA-man [Lactobacillus curvatus]	52	31
345	9	8348	9397	gi|606292	ORF_o696 [Escherichia coli]	52	27
398	3	2671	1877	gi|144859	ORF B [Clostridium perfringens]	52	29
411	1	992	3	gnl|PID|e283950	daunorubicin resistance ATP-binding protein DrrA [Sulfolobus solfataricus]	52	27
422	2	1292	585	gi|537214	yjjG gene product [Escherichia coli]	52	32
436	2	1669	1205	gi|507323	ORF1 [Bacillus stearothermophilus]	52	29
450	1	119	754	gi|1573916	multidrug resistance protein (emrB) [Haemophilus influenzae]	52	32
453	1	190	381	gi|182021	elastin [Homo sapiens]	52	40
455	7	5767	4634	gnl|PID|e155312	integrase [Bacteriophage TP901-1]	52	34
479	1	138	758	gi|1742859	ORF_ID:o327#7; similar to [SwissProt Accession Number P54449] [Escherichia coli]	52	27
517	1	763	2	gi|152780	rhamnosyl transferase II [Shigella dysenteriae]	52	29
518	3	1735	848	gi|153858	wall-associated protein [Streptococcus mutans]	52	20
526	3	2297	1848	gi|147402	mannose permease subunit III-Man [Escherichia coli]	52	27
617	1	1	462	gi|142863	replication initiation protein [Bacillus subtilis]	52	35
639	3	1068	259	gi|1591153	hypothetical protein (SP:P46348) [Methanococcus jannaschii]	52	30
703	1	773	81	gi|793910	surface antigen [Homo sapiens]	52	31

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
737	1	235	2	gi|666000	hypothetical protein [Bacillus subtilis]	52	29
791	4	1368	1802	gnl|PID|e269549	Unknown [Bacillus subtilis]	52	28
825	1	1	300	gi|732538	No definition line found [Caenorhabditis elegans]	52	28
981	1	226	2	gi|951100	P45016a-ms1 [Mus spretus]	52	36
17	23	23542	22163	gi|1652483	hypothetical protein [Synechocystis sp.]	51	32
65	6	4302	3691	gi|397498	Membrane Ribose Binding Protein [Bacillus subtilis] pir|S42714|S42714 membrane ribose-binding protein - Bacillus ubtilis	51	31
69	5	2926	2537	gi|1773150	hypothetical 14.8kd protein [Escherichia coli]	51	30
92	1	973	44	gnl|PID|e243523	ORF YGR130c [Saccharomyces cerevisiae]	51	29
103	6	5272	3593	gi|312940	threonine kinase [Streptococcus equisimilis]	51	32
111	7	4195	3317	pir|G64143|G64143	hypothetical protein HI0143 - Haemophilus influenzae (strain Rd KW20)	51	29
115	7	4526	3414	gi|405879	yeiH [Escherichia coli]	51	27
123	29	27788	28207	gi|147402	mannose permease subunit III-Man [Escherichia coli]	51	27
125	1	223	2	gi|4482	SLY1 gene product [Saccharomyces cerevisiae]	51	37
128	21	16156	15638	gi|606026	ORF_o115 [Escherichia coli]	51	27
137	4	3207	5369	gi|1673692	(AE000005) Mycoplasma pneumoniae, C09_orf422 Protein [Mycoplasma pneumoniae]	51	26
138	28	18295	18771	gi|149647	ORFZ [Listeria monocytogenes]	51	31
145	6	4054	5271	gi|1653860	N-acyl-L-amino acid amidohydrolase [Synechocystis sp.]	51	41
155	4	3019	2273	gi|1486242	unknown [Bacillus subtilis]	51	41
180	8	7951	9189	gi|1657522	hypothetical protein [Escherichia coli]	51	32
186	2	859	1620	gi|511497	oleoyl-acyl carrier protein thioesterase [Coriandrum sativum]	51	29

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
186	3	1644	2060	sp|P37348|YECE_ECOLI	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	51	38
194	3	1521	1276	gi|332697	fusion protein [Human parainfluenza virus 2]	51	32
195	7	1986	3767	gi|405570	TraK protein shares sequence similarity with a family of proteins ncoded on Gram-negative gene transfer systems such as TraD from the plasmid [Plasmid pSK41]	51	28
197	1	3	494	gi|1592234	DNA topoisomerase I [Methanococcus jannaschii]	51	32
198	2	1521	862	gi|1196483	unknown protein [Lactobacillus casei]	51	32
238	16	13630	14730	gi|1772652	2-keto-3-deoxygluconate kinase [Haloferax alicantei]	51	36
257	5	5646	4513	pir|S43367|S43367	metallothionein - Green crab, common shore crab	51	38
261	6	4950	4519	gi|581545	orf 4 [Staphylococcus aureus]	51	26
270	5	4480	4220	gi|1066975	F49E2.5a [Caenorhabditis elegans]	51	28
306	10	5928	6905	gi|1752736	gene required for phosphoylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	51	28
324	3	1590	2405	gi|409925	VirR positive regulator [Streptococcus pyogenes]	51	25
328	2	632	309	gi|466475	putative phospho-beta-glucosidase [Bacillus stearothermophilus] pir|D49898|D49898 cellobiose phosphotransferase system celC - acillus stearothermophilus	51	30
340	2	898	1152	gi|40046	phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus] ir|S15936|NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	51	39

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
340	4	3617	2445	gi|763052	integrase [Bacteriophage T270]	51	33
379	10	11742	11311	gi|887829	D21141 uses 2nd start; frame determined by Lac fusion [Escherichia oli]	51	34
380	1	2	1123	gi|309662	pheromone binding protein [Plasmid pCF10]	51	34
395	1	526	95	gi|490986	phi 105 repessor orf2 [unidentified]	51	27
424	4	2512	995	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	51	31
444	1	737	483	gi|1245376	cardiac ryanodine receptor [Oryctolagus cuniculus]	51	34
483	1	1	642	gi|1303981	YqkD [Bacillus subtilis]	51	29
500	1	2	550	gi|987094	membrane transport protein [Streptomyces hygroscopicus]	51	23
525	3	492	983	pir|A57438|A57438	tryptophan-rich sensory protein - Rhodobacter sphaeroides (strain 2.4.1)	51	38
534	1	2	1165	gi|147516	ribokinase [Escherichia coli]	51	33
547	1	1	387	gi|1353528	ORF11 [Bacteriophage r1t]	51	33
553	2	1728	1330	pir|B55124|B55124	thioredoxin - Chlorobium sp.	51	27
574	1	2291	2476	bbs|129435	RprX=inner membrane signal-transducing protein [Bacteroides fragilis, Peptide, 519 aa] [Bacteroides fragilis]	51	36
574	2	3145	3420	gi|1732202	PTS permease for mannose subunit IIIMan N terminal domain [Vibrio furnissii]	51	29
594	2	530	225	gi|1657696	tryptophan hydroxylase [Gallus gallus]	51	40
605	3	1220	1936	gnl|PID|e289149	similar to B. subtilis YcsE hypothetical protein [Bacillus subtilis]	51	32
609	1	1027	74	gi|1226279	strong similarity to Schistosoma amino acid permease (GB:L25068) [Caenorhabditis elegans]	51	26
656	2	2033	2950	gi|143213	putative [Bacillus subtilis]	51	26
670	1	1508	369	gi|1652222	hypothetical protein [Synechocystis sp.]	51	25

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
673	1	2	1135	gi|532553	ORF20 [Enterococcus faecalis]	51	27
674	2	1158	778	gi|467451	unknown [Bacillus subtilis]	51	26
735	2	477	725	gi|757791	aromatic amino acid permease [Corynebacterium glutamicum] pir|S52754|S52754 aromatic amino acid permease - Corynebacterium lutamicum	51	38
924	1	794	3	gi|40663	sialidase [Clostridium septicum]	51	35
4	5	3811	4728	gi|413948	ipa-24d gene product [Bacillus subtilis]	50	29
8	3	3310	2180	gi|1592205	M. jannaschii predicted coding region MJ1595 [Methanococcus jannaschii]	50	28
11	9	5269	5520	gi|1651800	L-glutamine:D-fructose-6-P amidotransferase [Synechocystis sp.]	50	25
12	6	9045	8662	gnl|PID|e254943	unknown [Mycobacterium tuberculosis]	50	23
15	4	2911	4269	gi|1592173	N-ethylammeline chlorohydrolase [Methanococcus jannaschii]	50	28
19	10	4934	5530	gi|825569	unknown [Saccharomyces cerevisiae]	50	20
28	5	7515	7057	gi|1230586	orf10; Method: conceptual translation supplied by author [Vibrio cholerae O139]	50	38
45	9	4279	5019	gi|1591029	thioredoxin/glutaredoxin [Methanococcus jannaschii]	50	32
54	16	7739	7590	gi|1589837	cuticle preprocollagen [Meloidogyne incognita]	50	46
59	5	1551	2345	gi|144297	acetyl esterase (XynC) [Caldocellum saccharolyticum] pir|B37202|B37202 acetylesterase (EC 3.1.1.6) (XynC) - Caldocellum accharolyticum	50	34
62	3	1650	1360	gnl|PID|e205266	LEA76 homologue type2 [Arabidopsis thaliana]	50	31
91	10	8858	7521	gi|758229	integrase [Bacteriophage phi-13]	50	31
112	5	3548	2133	gi|1184262	GadC [Shigella flexneri]	50	25
123	13	13099	14319	gi|178273	alanine:glyoxylate aminotransferase [Homo sapiens]	50	31

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
123	15	14395	15675	gi|467342	unknown [Bacillus subtilis]	50	28
123	31	28700	29494	gi|43942	first subunit of EII-Sor [Klebsiella pneumoniae]	50	27
124	2	1666	1061	gi|556016	similar to plant water stress proteins; ORF2 [Bacillus subtilis] gi|556016 similar to plant water stress proteins; ORF2 [Bacillus ubtilis]	50	34
128	39	32767	31829	gi|39993	UDP-N-acetylmuramoylalanine--D-glutamate ligase [Bacillus subtilis]	50	33
135	11	8803	7694	gi|895747	putative cel operon regulator [Bacillus subtilis]	50	26
138	21	14648	13653	gi|1591472	malic acid transport protein [Methanococcus jannaschii]	50	26
146	3	2338	1415	gi|1732200	PTS permease for mannose subunit IIPMan [Vibrio furnissii]	50	27
160	2	724	1302	gnl|PID|e264218	F54F3.4 [Caenorhabditis elegans]	50	30
164	15	15432	16364	gi|409286	bmrU [Bacillus subtilis]	50	27
167	9	17082	15394	gi|143156	membrane bound protein [Bacillus subtilis]	50	30
179	3	2350	4485	gi|1408485	yxdM gene product [Bacillus subtilis]	50	24
180	30	31056	30643	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	50	27
184	1	2	1015	gi|854232	cymE gene product [Klebsiella oxytoca]	50	24
194	7	4335	4817	gi|1256652	25% identity to the E.coli regulatory protein MprA; putative [Bacillus subtilis]	50	30
195	29	11712	12422	gi|662263	ORF5 [Plasmid pIP501]	50	25
204	1	2	166	gi|328656	envelope polyprotein [Human immunodeficiency virus type 1]	50	45
205	7	3118	3861	gi|437697	traE [Plasmid RP4]	50	31
216	11	7181	7750	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	50	30
223	10	7036	8082	gi|606423	T09B9.1 [Caenorhabditis elegans]	50	30

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
223	22	19257	19799	gi|1256141	YbbL [Bacillus subtilis]	50	29
233	4	3102	2320	gi|887826	GUG start [Escherichia coli]	50	32
238	6	5102	3906	gi|1161219	homolgous to D-amino acid dehydrogenase enzyme [Pseudomonas aeruginosa]	50	29
239	3	4449	5159	gi|41519	P30 protein (AA 1-240) [Escherichia coli]	50	31
242	2	147	2210	gi|160299	glutamic acid-rich protein [Plasmodium falciparum] pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum	50	30
248	2	263	712	gi|143725	putative [Bacillus subtilis]	50	32
256	8	8531	7395	gnl|PID|e250452	C44H9.4 [Caenorhabditis elegans]	50	38
265	3	1150	893	gi|1402527	ORF6 [Enterococcus faecalis]	50	39
276	24	14203	14000	gi|1591019	M. jannaschii predicted coding region MJ0297 [Methanococcus jannaschii]	50	33
276	32	20601	19924	gi|1334905	BXLF2 late reading frame, encodes gp85; homologous to RF 37 VZV and glycoprotein H of HSV (gpIII of VZV) [Human herpesvirus 4]	50	29
286	1	1	747	gnl|PID|e257895	homology with truncated ORF2 of pepF2 [Lactococcus lactis]	50	32
301	17	11706	13313	gi|562039	NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii] pir|S53835|S53835 NADH dehydrogenase chain 2 - Acanthamoeba astellanii mitochondrion (SGC6)	50	26
338	5	2206	3729	gi|829194	bacterial cell wall hydrolase [Enterococcus faecalis] pir|A38109|A38109 autolysin - Enterococcus faecalis sp|P37710|ALYS_ENTFA AUTOLYSIN (EC 3.5.1.28) N-ACETYLMURAMOYL-L-ALANINE AMIDASE).	50	34
345	12	11781	13379	gnl|PID|e235181	unknown [Mycobacterium tuberculosis]	50	32

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
360	2	2879	408	gi|40782	bps2 gene product [Desulfurolobus ambivalens]	50	25
372	1	6	440	gi|1552733	similar to voltage-gated chloride channel protein [Escherichia coli]	50	31
372	2	391	738	gi|1591749	TRK system potassium uptake protein A [Methanococcus jannaschii]	50	23
377	3	2262	1846	gi|52797	kinesin heavy chain [Mus musculus]	50	22
392	1	433	2	gi|147213	phnP protein [Escherichia coli]	50	33
399	31	29803	30186	gi|146288	PTS enzyme III glucitol [Escherichia coli]	50	30
518	4	2885	2040	gi|475107	regulatory protein [Pediococcus pentosaceus]	50	29
528	1	3	665	gi|215098	excisionase [Bacteriophage 154a]	50	38
562	1	631	107	gi|1592205	M. jannaschii predicted coding region MJ1595 [Methanococcus jannaschii]	50	28
596	1	227	1153	gi|963039	orf gene product [Enterococcus hirae]	50	26
680	1	2	1090	gi|1050297	product p150Glued [Neurospora crassa]	50	27
755	1	2	430	gi|1736469	Tetracenomycin C resistance and export protein. [Escherichia coli]	50	33
838	1	428	3	gi|530424	50S ribosomal protein [Mycoplasma capricolum]	50	30
14	2	3453	538	gi|47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis] ir|S10223|HMSO1F aggregation protein asa1 - Enterococcus faecalis asmid pAD1	49	25
56	7	5367	4822	gi|924754	glycine reductase complex selenoprotein B [Clostridium litorale]	49	31
68	9	4741	7389	gi|1591494	M. jannaschii predicted coding region MJ0797 [Methanococcus jannaschii]	49	21
94	10	9425	6633	gi|1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis]	49	30
98	12	12306	11701	gi|1303784	YqeD [Bacillus subtilis]	49	26

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
117	7	4789	6228	gi|435493	orf4 gene product [Lactococcus lactis]	49	26
123	21	18576	19745	gi|298032	EF [Streptococcus suis]	49	29
125	4	2358	1594	gnl|PID|e237295	unknown [Saccharomyces cerevisiae]	49	27
125	6	4235	3453	gi|1573885	glycosyl transferase (lgtD) [Haemophilus influenzae]	49	32
144	5	3715	4062	gi|507130	emm64 gene product [Streptococcus pyogenes]	49	30
162	8	10472	9120	gi|47045	NADH oxidase [Enterococcus faecalis]	49	34
179	18	18426	17848	gi|40060	DNA polymerase III (AA 1-1437) [Bacillus subtilis] p|P13267|DP3A_BACSU DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7).	49	27
180	19	18727	19917	gi|143000	proton glutamate symport protein [Bacillus stearothermophilus] pir|S26247|S26247 glutamate/aspartate transport protein - Bacillus tearothermophilus	49	31
224	1	145	1371	gi|1103862	TolA [Pseudomonas aeruginosa]	49	32
236	8	10955	9249	gi|431272	lysis protein [Bacillus subtilis]	49	28
278	1	757	2	gi|467478	unknown [Bacillus subtilis]	49	29
290	8	6860	7366	gi|466875	nifU; B1496_C1_157 [Mycobacterium leprae]	49	35
318	5	4065	3190	gi|144859	ORF B [Clostridium perfringens]	49	25
318	8	6052	5033	gi|1439528	EIIC-man [Lactobacillus curvatus]	49	30
335	1	534	40	gi|216861	24K membrane protein [Pseudomonas aeruginosa]	49	24
338	4	2861	2169	gnl|PID|e288536	F37H8.a [Caenorhabditis elegans]	49	30
346	4	1257	2273	gi|536970	ORF_f543 [Escherichia coli]	49	25
355	20	12902	15262	gi|292836	trichohyalin [Homo sapiens]	49	20
366	1	1	1437	gi|405857	yehU [Escherichia coli]	49	26
375	8	7663	6470	gi|1573546	H. influenzae predicted coding region HI0561 [Haemophilus influenzae]	49	30
377	2	1624	392	gi|532553	ORF20 [Enterococcus faecalis]	49	27
399	5	3960	3142	gi|1742362	nta operon transcriptional regulator.	49	29

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Escherichia coli]		
456	1	1070	342	gi|290533	similar to E. coli ORF adjacent to suc operon; similar to gntR class f regulatory proteins [Escherichia coli]	49	27
619	1	2	232	gi|665956	ribosomal protein S20 homolog [Aeromonas sobria] sp|P45786|RS20_AERHY 30S RIBOSOMAL PROTEIN S20 (FRAGMENT). sp|P45788|RS20_AERSO 30S RIBOSOMAL PROTEIN S20 (FRAGMENT).	49	41
621	1	319	942	gi|149456	nisin-resistance protein [Lactococcus lactis]	49	29
630	1	3	1190	gi|537145	ORF_f437 [Escherichia coli]	49	34
736	1	859	2	gi|1592020	hypothetical protein (SP:P37555) [Methanococcus jannaschii]	49	27
849	1	232	11	gi|145514	cyclopropane fatty acid synthase [Escherichia coli]	49	35
47	11	14140	13307	gi|1045937	M. genitalium predicted coding region MG246 [Mycoplasma genitalium]	48	34
103	4	2492	1605	gi|1591514	membrane protein [Methanococcus jannaschii]	48	19
127	7	6836	5736	gi|1573128	hypothetical [Haemophilus influenzae]	48	24
138	22	14742	15590	gi|580884	ipa-89d gene product [Bacillus subtilis]	48	33
160	6	3048	3665	gi|1652295	serine esterase [Synechocystis sp.]	48	28
162	3	3048	2491	gi|143830	xpaC [Bacillus subtilis]	48	13
193	2	1257	310	gi|1591153	hypothetical protein (SP:P46348) [Methanococcus jannaschii]	48	24
219	1	61	573	gnl|PID|e257628	ORF [Lactococcus lactis]	48	32
221	11	5952	6428	gi|1303733	YqaN [Bacillus subtilis]	48	31
232	4	2776	1712	gi|142707	comG2 gene product [Bacillus subtilis]	48	24
236	6	8618	7689	gi|550075	cephalosporin-C deacetylase [Bacillus subtilis]	48	26
238	28	25896	26825	gi|47906	rha regulatory protein [Salmonella	48	31

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					typhimurium]		
251	2	1935	640	gi|1143026	ORF10 [Spiroplasma virus]	48	30
252	1	2036	3	gnl|PID|e228699	homologous to yqbO of the skin element [Bacillus subtilis]	48	37
269	1	481	2	gi|1045975	sensory rhodopsin II transducer [Mycoplasma genitalium]	48	28
315	5	4604	2649	gi|396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp|P32703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549).	48	30
327	1	128	916	gi|216314	esterase [Bacillus stearothermophilus]	48	30
330	6	4486	5337	gi|43942	first subunit of EII-Sor [Klebsiella pneumoniae]	48	21
330	7	5325	6230	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	48	33
345	10	9571	10521	gi|1736789	Collagenase precursor (EC 3.4.-.-). [Escherichia coli]	48	26
509	1	1	444	gi|606376	ORF_o162 [Escherichia coli]	48	33
531	1	624	109	sp|P50848|YPWA_BACSU	HYPOTHETICAL 58.2 KD PROTEIN IN KDGT-XPT INTERGENIC REGION.	48	33
549	3	962	369	gi|1001212	molybdenum cofactor biosynthesis protein C [Synechocystis sp.]	48	32
725	1	3	500	gi|1151158	repeat organellar protein [Plasmodium chabaudi]	48	25
789	1	133	717	gi|42724	rhaS (AA 1-278) [Escherichia coli]	48	39
936	1	32	316	gi|532549	ORF16 [Enterococcus faecalis]	48	45
2	2	2662	449	gi|929878	J1027 gene product [Saccharomyces cerevisiae]	47	20
4	2	1002	2192	gi|763052	integrase [Bacteriophage T270]	47	29
21	8	6350	5355	gi|1066343	mu-crystallin [Homo sapiens]	47	29
25	3	915	2048	gi|1064813	homologous to sp:PHOR_BACSU [Bacillus subtilis]	47	21

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
59	2	953	1378	gi|872306	integral membrane protein [Streptomyces pristinaespiralis] pir|S57509|S57509 integral membrane protein - Streptomyces ristinaespiralis	47	26
81	7	4970	4206	gi|1591754	hypothetical protein (SP:P39364) [Methanococcus jannaschii]	47	22
82	3	1534	866	gi|397526	clumping factor [Staphylococcus aureus]	47	21
110	5	2313	3767	gi|151928	48 kDa protein [Rhodobacter sphaeroides]	47	26
150	11	7839	9107	gnl|PID|e275490	C30H6.k [Caenorhabditis elegans]	47	16
161	2	116	1450	gnl|PID|e283830	aminotransferase [Sulfolobus solfataricus]	47	23
165	8	8081	6129	gi|924925	heparinase III protein [Cytophaga heparina]	47	29
180	31	31515	31054	gi|1591753	N-acetylglucosamine-1-phosphate transferase [Methanococcus jannaschii]	47	29
194	11	8247	9236	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	47	26
225	2	1039	701	gi|1212992	Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo sapiens]	47	33
232	1	196	969	gi|293033	integrase [Bacteriophage phi-LC3]	47	30
232	6	3687	3340	gi|142706	comG1 gene product [Bacillus subtilis]	47	28
233	10	8424	6739	gi|887816	possible start 13 codons upstream, for o765 [Escherichia coli]	47	35
346	2	706	1083	gi|536970	ORF_f543 [Escherichia coli]	47	27
352	1	112	843	gi|1591857	H+-transporting ATPase [Methanococcus jannaschii]	47	28
410	1	3	980	gi|1652869	NADH dehydrogenase [Synechocystis sp.]	47	30
465	2	1976	1749	gi|211659	p68 protein; c-rel proto-oncogene [Gallus gallus]	47	30
491	3	3752	2466	gi|881434	ORFP [Bacillus subtilis]	47	24
501	1	48	809	gi|467429	unknown [Bacillus subtilis]	47	33

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
532	1	3	287	gi|755724	alpha-toxin [Clostridium novyi]	47	32
578	1	707	81	gi|532547	ORF14 [Enterococcus faecalis]	47	30
605	4	2051	2470	gi|1783233	hypothetical [Bacillus subtilis]	47	22
626	3	2459	2169	gi|1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus influenzae]	47	44
650	1	1042	341	gi|404802	integrase [Saccharopolyspora erythraea]	47	26
665	1	714	1175	gi|143655	sporulation protein [Bacillus subtilis]	47	22
754	2	1086	736	gi|143835	PBSX repressor [Bacillus subtilis]	47	27
845	1	2	241	gi|1303952	YqjA [Bacillus subtilis]	47	26
911	1	1	456	gi|1019640	ORFX (a homolog to the prgX gene of the pheromone response plasmid pCF10); putative [Plasmid pHKK701]	47	26
933	1	16	303	gi|331002	first methionine codon in the ECLF1 ORF [Saimiriine herpesvirus 2] gi|60394 ORF 73; ECLF1 [Saimiriine herpesvirus 2]	47	29
17	17	13073	13675	gi|1304597	abortive phage resistance protein [Lactococcus lactis]	46	27
19	11	5515	6393	gi|1353529	ORF12 [Bacteriophage r1t]	46	28
42	3	2460	3011	gi|1064814	homologous to sp:PHOP_BACSUB [Bacillus subtilis]	46	33
49	9	4042	5793	gnl|PID|e59644	predicted 86.4kd protein; 52Kd observed [Mycobacteriophage 15]	46	22
74	6	4039	3434	gi|143542	RNA polymerase sigma-30 factor [Bacillus licheniformis] pir|B28625|SZBSSL transcription initiation factor sigma H - acillus licheniformis	46	27
89	14	14259	12967	gi|1499089	M. jannaschii predicted coding region MJ0305 [Methanococcus jannaschii]	46	32
89	15	15737	14427	gi|1653339	hypothetical protein [Synechocystis sp.]	46	22
94	13	12634	11132	gi|1402515	membrane-spanning transporter protein [Clostridium perfringens]	46	23

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
100	18	13493	11958	gi|15470	portal protein [Bacteriophage SPP1]	46	31
144	2	2364	1126	gnl|PID|e183450	hypothetical EcsB protein [Bacillus subtilis]	46	25
144	9	8977	6236	gi|710421	unknown [Staphylococcus aureus]	46	24
152	7	3397	4557	gnl|PID|e254991	hypothetical protein [Bacillus subtilis]	46	25
158	7	7144	5993	gi|1045800	ribose transport system permease protein [Mycoplasma genitalium]	46	28
180	11	10882	10055	gi|303953	esterase [Acinetobacter calcoaceticus]	46	23
181	3	1173	976	gi|1591638	M. jannaschii predicted coding region MJ0975 [Methanococcus jannaschii]	46	36
240	1	715	221	gi|1766062	Ats1 [Schizosaccharomyces pombe]	46	28
254	2	499	2	gi|153661	translational initiation factor IF2 [Enterococcus faecium] sp|P18311|IF2_ENTFC INITIATION FACTOR IF-2.	46	32
262	4	5276	4431	pir|A45605|A45605	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	46	20
309	1	2	673	gi|1651714	type 4 prepilin peptidase [Synechocystis sp.]	46	40
312	1	18	872	gi|580884	ipa-89d gene product [Bacillus subtilis]	46	32
324	6	4450	4836	gi|1061418	ArsC [Plasmid R46]	46	28
345	1	2241	1333	gi|144859	ORF B [Clostridium perfringens]	46	24
386	4	1438	2421	gi|405894	1-phosphofructokinase [Escherichia coli]	46	31
395	8	3584	3853	gnl|PID|e120267	sucrose-phosphate synthase [Beta vulgaris]	46	25
491	2	2527	1169	gnl|PID|e267595	Unknown, similar to peptidases [Bacillus subtilis]	46	29
495	3	612	869	gi|406286	triose phosphate/phosphate translocator [Flaveria pringlei] pir|S37553|S37553 triose phosphate/3-phosphoglycerate/phosphate ranslocator - Flaveria pringlei	46	27
513	1	2	946	gi|143024	glucose-resistance amylase regulator	46	26

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Bacillus subtilis] pir|S15318|S15318 ccpA protein - Bacillus subtilis sp|P25144|CCPA_BACSU GLUCOSE-RESISTANCE AMYLASE REGULATOR CATABOLITE CONTROL PROTEIN).		
520	3	914	2674	gi|1163086	microfilarial sheath protein SHP3 [Brugia malayi]	46	27
554	1	3	788	gi|413972	ipa-48r gene product [Bacillus subtilis]	46	27
568	1	1574	3	gi|532549	ORF16 [Enterococcus faecalis]	46	28
809	1	506	135	gi|49021	surface exclusion protein (SEA1) [Enterococcus faecalis] ir|S22452|S22452 surface exclusion protein sea1 precursor - terococcus faecalis plasmid pAD1	46	28
813	1	2	1090	gi|150556	surface protein [Plasmid pCF10]	46	34
78	2	4915	2516	gi|577295	The ha1225 gene product is related to human alpha-glucosidase. [Homo apiens]	45	20
81	9	6123	5386	gi|147200	phnF protein [Escherichia coli]	45	28
85	1	120	761	gi|457514	gltC [Bacillus subtilis]	45	19
94	11	10681	9668	gi|289753	homology with nucleolin protein; putative [Caenorhabditis elegans] pir|S44897|S44897 ZK1236.2 protein - Caenorhabditis elegans sp|P34618|YO82_CAEEL HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN HROMOSOME III.	45	23
108	3	2427	1789	gnl|PID|e263931	OrfD [Streptococcus pneumoniae]	45	27
108	4	3338	2352	gi|606150	ORF_f309 [Escherichia coli]	45	25
131	6	3981	5309	gi|1590845	hypothetical protein (PIR:S51413) [Methanococcus jannaschii]	45	36
144	11	10215	8944	gi|1001554	hypothetical protein [Synechocystis sp.]	45	30
164	11	8247	6736	gi|409925	VirR positive regulator [Streptococcus pyogenes]	45	22
192	1	1598	591	gi|1736826	Lysozyme M1 precursor (EC 3.2.1.17) (1,4-b-N-acetylmuramidase M1). [Escherichia	45	27

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					coli]		
223	16	14409	15212	gi|1651958	hypothetical protein [Synechocystis sp.]	45	32
279	7	5236	5772	gi|1736514	Isochorismatase (EC 3.3.2.1) (2,3 dihydro-2,3 dihydroxybenzoate synthase). [Escherichia coli]	45	29
364	3	2419	4098	gi|309662	pheromone binding protein [Plasmid pCF10]	45	26
459	1	2	307	gi|1679640	ORFA [Mycoplasma mycoides mycoides SC]	45	27
491	1	1022	135	sp|P27434|YFGA_ECOLI	HYPOTHETICAL 36.2 KD PROTEIN IN NDK-GCPE INTERGENIC REGION.	45	20
496	1	847	2	gi|1208489	serum resistance locus BrkB [Synechocystis sp.]	45	19
542	2	1169	804	gi|1064811	function unknown [Bacillus subtilis]	45	28
63	3	1047	1919	gi|39848	U3 [Bacillus subtilis]	44	26
93	3	1108	1374	sp|Q04747|SRF2_BACSU	SURFACTIN SYNTHETASE SUBUNIT 2.	44	27
155	10	8354	7620	sp|P35136|SERA_BACSU	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).	44	29
215	2	2192	1134	gi|468760	ORF334 [Rhizobium meliloti]	44	31
303	1	466	2	gi|431950	similar to a B.subtilis gene (GB: BACHEMEHY_5) [Clostridium asteurianum]	44	22
310	1	284	39	pir|S01294|S01294	intermediate filament protein B - Roman snail	44	26
311	1	122	2668	gi|532549	ORF16 [Enterococcus faecalis]	44	27
320	1	709	2	gi|290801	member of super-family of ABC proteins [Francisella tularensis (var. ovicida)]	44	23
341	14	13882	12998	gi|142863	replication initiation protein [Bacillus subtilis]	44	16
345	15	16445	18001	gi|151282	DL-hydantoinase [Pseudomonas sp.]	44	34
386	3	1340	570	sp|P46117|YARA_PROST	HYPOTHETICAL 31.5 KD PROTEIN IN AARA 3'REGION.	44	19
862	1	483	4	gi|929796	precursor of the major merozoite surface	44	26

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					antigens [Plasmodium alciparum]		
19	3	1695	1372	gi|603263	Yel055p [Saccharomyces cerevisiae]	43	31
45	17	14045	14995	gnl|PID|e233895	hypothetical protein [Bacillus subtilis]	43	32
57	1	667	317	gi|664840	TagB [Dictyostelium discoideum]	43	22
71	2	1537	2568	gi|1303981	YqkD [Bacillus subtilis]	43	26
72	18	20511	20164	gi|349045	merozoite surface antigen 2 [Plasmodium falciparum]	43	36
94	9	6581	6039	gi|1146245	putative [Bacillus subtilis]	43	28
180	17	16391	17656	gi|290540	f445 [Escherichia coli]	43	24
252	2	2407	1829	gi|154381	chemoreceptor [Salmonella typhimurium]	43	19
276	30	19091	18480	gi|15470	portal protein [Bacteriophage SPP1]	43	23
311	2	2666	4639	gi|160299	glutamic acid-rich protein [Plasmodium falciparum] pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum	43	28
631	2	1126	2328	gi|1519696	coded for by C. elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 [Caenorhabditis elegans]	43	27
11	3	1509	2342	gi|143150	levR [Bacillus subtilis]	42	21
45	14	10730	12028	gi|666069	orf2 gene product [Lactobacillus leichmannii]	42	23
72	19	21070	21981	gnl|PID|e236595	orf7 gene product [Enterococcus faecalis]	42	23
123	35	32205	32768	gi|1772652	2-keto-3-deoxygluconate kinase [Haloferax alicantei]	42	27
136	5	2737	2375	gi|153858	wall-associated protein [Streptococcus mutans]	42	27
167	4	2701	6540	gi|1519696	coded for by C. elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5	42	27

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
					[Caenorhabditis elegans]		
195	31	12430	13155	pir|S33124|S33124	tpr protein - human	42	24
211	1	187	2	gi|1653346	GDP-mannose pyrophosphorylase [Synechocystis sp.]	42	33
242	13	8089	12447	gi|951460	FIM-C.1 gene product [Xenopus laevis]	42	31
305	5	4354	5340	gi|1408485	yxdM gene product [Bacillus subtilis]	42	25
355	18	9964	12549	gi|532549	ORF16 [Enterococcus faecalis]	42	30
446	4	4428	5261	gi|47528	glucosyltransferase S [Streptococcus salivarius]	42	25
656	3	2866	3456	gi|142857	MreD protein [Bacillus subtilis]	42	25
686	11	3646	3921	pir|A44805|A44805	eggshell protein - fluke (Schistosoma haematobium) (subclone SH.E 2-1)	42	42
920	1	41	316	gi|532549	ORF16 [Enterococcus faecalis]	42	40
23	3	729	487	gi|414525	meiotin-1 [Lilium longiflorum]	41	41
56	5	3511	2324	gi|1591610	probable ATP-dependent helicase [Methanococcus jannaschii]	41	21
98	17	16843	16274	gi|1742129	Immunity repressor protein. [Escherichia coli]	41	23
167	6	6734	9811	gnl|PID|e249616	F56H9.1 [Caenorhabditis elegans]	41	37
171	13	10879	11871	gi|331002	first methionine codon in the ECLF1 ORF [Saimiriine herpesvirus 2] gi|60394 ORF 73; ECLF1 [Saimiriine herpesvirus 2]	41	23
181	2	1012	500	gi|455315	ORF 4 [Plasmid pIP404]	41	24
230	4	3664	3224	gi|498251	glutamate/aspartate transporter II [Homo sapiens]	41	22
718	1	2	613	gi|984656	ORF3 [Salmonella typhimurium]	41	22
19	30	16391	17770	gi|806704	Upf2p [Saccharomyces cerevisiae]	40	21
164	16	16440	17951	gi|348056	trans-acting positive regulator [Bacillus anthracis]	40	22
200	12	5956	4841	gi|1574243	H. influenzae predicted coding region HI1405 [Haemophilus influenzae]	40	24

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
216	10	6799	7194	gi|146279	glucitol-specific enzyme III (gutB) [Escherichia coli]	40	27
292	13	8633	10741	gi|1008233	ORF YJL076w [Saccharomyces cerevisiae]	40	18
345	13	14050	15333	gi|581051	cytosine permease [Escherichia coli]	40	25
521	1	177	1466	gi|289614	homology with glucose induced repressor, GRR1; putative Caenorhabditis elegans]	40	18
64	3	2646	1855	gi|154924	spectinomycin adenyltransferase [Transposon Tn554]	39	27
100	17	12037	10565	gi|1052806	product required for head morphogenesis [Bacteriophage SPP1]	39	24
529	1	326	4939	gi|295671	selected as a weak suppressor of a mutant of the subunit AC40 of DNA ependant RNA polymerase I and III [Saccharomyces cerevisiae]	39	19
49	2	518	931	gi|166162	Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11]	38	19
54	19	11264	10854	gi|160186	circumsporozoite protein [Plasmodium vivax]	38	31
164	21	22793	23587	gi|603857	secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]	38	18
167	3	2322	2756	gi|435039	proline-rich cell wall protein [Gossypium hirsutum]	38	36
204	2	133	798	gi|396401	No definition line found [Escherichia coli]	38	25
475	2	761	1792	gi|1574532	H. influenzae predicted coding region HI1680 [Haemophilus influenzae]	38	27
164	19	20738	21385	gi|165704	[Rabbit smooth muscle myosin light chain kinase mRNA, complete DS.], gene product [Oryctolagus cuniculus]	37	20
394	6	5649	6395	gi|603857	secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]	36	16
958	1	1	459	gi|951460	FIM-C.1 gene product [Xenopus laevis]	36	28

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% Sim	% Ident
399	21	16383	21359	gi|1707247	partial CDS [Caenorhabditis elegans]	34	13
150	12	9056	11740	gi|1015903	ORF YJR151c [Saccharomyces cerevisiae]	33	19
195	34	13017	15512	gi|632549	NF-180 [Petromyzon marinus]	33	18

Tabl 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
2	1	458	3
2	3	2208	2624
5	3	928	1440
8	6	4792	5877
8	7	5480	5262
12	1	2	832
12	2	771	4622
13	1	2	1684
14	1	531	130
15	2	862	1197
16	1	51	200
17	4	3309	3665
17	13	10079	10261
17	18	14431	13682
17	22	21525	21956
17	27	27055	27567
18	4	2172	1591
18	5	2524	2249
18	7	3467	3715
18	8	4082	3555
18	9	4333	4055
18	10	4395	4204
18	11	4498	4677
18	12	4656	5393
18	13	5878	5492
18	15	6296	6931
19	1	1047	676
19	2	1068	1247
19	4	1747	2031
19	5	2244	2612
19	7	2797	2943

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
19	9	3873	4730
19	13	6884	7420
19	14	7428	8042
19	16	9246	8425
19	17	9412	9615
19	19	9733	9918
19	20	10032	10334
19	21	10422	11009
19	22	11516	11944
19	24	12423	12881
19	26	14606	15427
19	27	15414	15848
19	28	15802	16134
19	29	16064	16393
19	32	17846	18052
19	33	18021	18356
19	34	18334	18684
19	35	18659	19036
19	36	18991	19677
19	37	19671	20132
19	39	22603	23337
19	40	23319	25580
21	2	762	262
21	5	3440	2925
21	10	7684	7241
23	5	2098	2652
23	8	4912	4709
23	9	4911	5246
23	10	5087	5353
23	22	14318	14926
23	23	14924	15565

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
23	24	15559	16083
23	29	17567	18022
25	2	553	1005
25	5	3363	2653
26	2	1220	1654
27	1	297	4
28	1	239	2833
29	5	3244	2822
29	6	4014	3301
29	7	4168	4557
29	8	5620	4595
32	3	2646	1375
32	4	2573	3010
39	9	4636	4986
40	2	1346	981
43	1	120	620
43	4	1972	2280
45	3	1557	1961
45	4	2012	2230
45	5	2218	2553
45	11	7226	5670
45	12	7270	10113
45	13	10013	10732
46	1	42	872
46	2	886	1125
46	4	2807	3100
47	4	5101	5625
47	10	13239	12847
49	1	106	504
49	8	2858	4132
49	10	5777	6193

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
49	11	6166	6720
52	5	3505	3110
52	7	5160	5603
52	8	5662	5459
54	2	400	729
54	4	1326	1610
54	5	2354	1335
54	6	1676	2080
54	7	2151	2576
54	12	4181	3954
54	13	5975	6289
54	14	6869	7144
54	15	7433	7107
54	18	9764	11086
55	2	252	440
56	2	1344	658
57	9	12450	12605
58	7	7066	6425
59	3	1350	952
59	4	1225	1515
59	7	2958	3200
62	6	4116	3007
63	1	77	364
63	2	455	1060
63	7	5422	5910
63	8	5870	6751
63	9	6688	7296
64	2	1849	1523
64	4	3183	2644
64	5	3422	3213
65	5	3787	3389

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
65	7	5043	4300
65	8	5354	4959
65	9	7005	6328
67	6	3719	4060
68	2	569	348
68	5	3234	2821
68	6	3808	3221
68	10	7495	8106
70	2	2102	1614
70	3	2019	2231
71	3	3362	3787
72	21	22464	22709
72	22	22690	23019
72	23	23013	23834
73	1	154	2
74	1	61	486
74	3	1334	1981
75	4	3227	2136
75	5	3994	3251
75	6	3348	3632
75	7	4519	4043
75	8	4296	4529
75	10	6518	5769
76	2	1079	1897
76	4	2113	2436
76	6	4737	4105
77	3	1874	2704
77	4	2665	2459
78	3	5814	5398
79	3	848	1645
79	4	2121	1642

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
81	8	5392	4961
81	13	8428	8874
81	21	15746	14802
82	1	858	4
82	2	198	383
83	3	2194	2604
83	4	2728	2405
83	6	2855	3172
83	10	7188	6184
83	11	7415	7065
83	17	12259	12561
83	21	15890	16456
83	23	16946	17251
84	5	7071	7949
85	7	6518	6174
89	2	1012	599
89	3	1382	939
89	4	2350	1370
89	5	2523	2314
89	9	7505	7182
89	16	15846	15673
89	19	20070	19045
90	1	3	689
91	7	3834	4127
91	8	4288	5268
91	9	7259	5748
91	12	9737	8973
91	13	10162	9731
92	3	1458	958
92	4	1934	1287
93	2	479	949

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
93	4	1344	1727
94	1	770	45
94	3	1460	1618
94	5	2279	1734
94	12	11000	10641
95	11	7674	7907
95	12	8604	8056
95	13	8725	8546
96	1	758	1018
96	2	1038	1469
98	5	6809	5994
98	10	10338	10652
98	11	10650	11558
99	2	232	513
100	4	3728	4048
100	6	5866	5378
100	7	6574	5921
100	8	6923	6534
100	9	7355	6921
100	10	7698	7339
100	11	8226	7744
100	13	9395	8514
100	15	10368	10102
100	19	14770	13505
100	20	15300	14758
100	21	15783	15298
100	23	17699	17292
100	25	20933	20625
100	26	21200	20946
100	28	23713	23156
100	29	23948	23691

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
100	30	24312	23965
100	31	24550	24287
100	32	24912	24565
100	33	25173	24910
100	34	26339	25158
100	36	27251	26994
100	37	27945	27232
100	39	28442	28227
100	40	28657	28403
100	46	30439	31146
100	47	31158	31712
101	2	850	464
101	3	2453	1899
102	6	5023	5616
102	9	6704	7111
103	7	5454	5296
105	2	1244	1828
106	4	5114	3294
106	6	7622	6168
106	7	6577	6867
108	6	5192	4158
110	1	2	454
110	6	3689	4207
110	9	9374	8553
110	10	9903	9361
110	11	10175	9843
111	6	3118	3267
112	4	2170	1043
114	2	1347	1135
116	8	4782	5147
117	4	2437	2670

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
117	6	3876	4640
117	8	5643	5927
117	9	6195	6488
117	12	9655	9837
119	1	3	500
119	2	670	1158
119	4	2730	2284
121	3	2276	3670
123	14	14304	14555
123	16	15305	15147
123	24	21896	22663
123	34	31458	32207
125	3	1581	1300
125	7	4516	4346
126	2	85	312
127	2	1047	787
127	3	2006	1299
127	4	3432	1924
128	4	3094	2747
128	5	3466	3305
128	6	4625	3507
128	7	4726	4550
128	13	8947	8522
128	15	9325	9582
128	17	10126	10380
128	24	17649	18038
129	1	276	1769
130	7	6478	6702
130	11	9386	9769
133	7	6622	7380
135	2	2289	1153

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
135	3	3380	2271
135	5	3778	3930
135	6	5835	5137
135	7	6649	5852
135	8	7021	6647
135	9	7420	7034
136	2	963	379
136	3	2009	939
136	4	2344	1973
138	4	5051	3636
138	11	8499	8753
138	12	8682	8536
138	13	8923	9270
138	14	9333	9887
138	15	9628	10308
138	16	10422	10216
138	23	15980	15678
138	24	16437	16063
138	30	19388	19828
139	3	1068	1466
139	4	3338	1983
139	5	3769	3317
139	6	4114	3818
139	7	4838	4236
139	10	5639	5175
142	1	369	106
142	2	1005	367
142	3	2140	980
142	4	2504	2127
142	5	2821	2474
142	6	3294	2806

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
142	7	4000	3635
143	1	650	3
143	3	1090	173
143	4	1044	433
144	10	7570	8403
144	12	10727	10335
145	1	188	30
145	2	775	978
150	9	6876	7166
150	13	11538	11242
152	1	35	445
152	2	405	914
152	3	912	1430
152	4	1349	2212
152	5	2210	2896
152	6	2739	3368
152	8	4479	4694
152	11	6647	7321
154	7	4557	4195
155	3	1227	2180
155	12	8726	9022
156	3	3179	2664
158	11	10876	11220
160	1	545	3
162	1	228	1349
162	2	2513	1653
162	7	9163	7664
162	9	10619	10990
162	11	11891	11427
163	3	1043	1234
163	5	3217	2021

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
163	6	3455	3198
163	8	5611	4931
163	9	5969	5580
163	10	6144	5926
164	2	1100	1687
164	9	5729	5259
164	10	6778	5639
164	12	8277	8450
164	17	18224	18526
164	24	24751	24536
164	27	25764	26369
165	1	17	481
165	2	2213	1389
165	12	9871	9689
165	14	11416	10367
166	3	1250	1669
167	5	3774	3439
167	7	10479	14498
167	10	17476	18768
168	2	665	393
172	9	7018	6701
172	10	7097	7930
173	1	2	412
173	3	2341	2024
173	6	4234	5055
173	9	7882	7295
173	10	7413	7571
173	14	12308	11748
174	4	2350	3021
174	5	3082	3498
178	3	866	1105

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
179	8	8115	7816
179	17	17407	17135
180	4	3524	4537
180	5	4686	5687
180	6	5897	6949
180	9	9721	9299
180	10	9996	9715
180	20	19805	19954
180	23	21808	21509
180	25	24127	26460
180	27	27977	27474
181	1	381	82
183	1	190	2
183	4	1849	2211
183	5	2350	2568
183	7	3592	2978
183	8	4176	3571
185	2	1260	1424
185	3	2722	1301
185	4	3612	2671
187	2	727	1302
187	3	1293	1745
187	5	2592	2173
189	1	18	2180
190	1	466	68
190	2	896	411
190	4	1878	2165
190	5	2740	2384
190	10	10281	8875
191	2	861	658
191	3	1096	827

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
192	2	1881	1564
193	1	316	2
193	7	4667	3813
194	1	30	641
194	2	608	1582
195	1	2	433
195	2	431	943
195	3	1055	465
195	4	972	1487
195	5	1507	1995
195	6	3314	1851
195	9	3089	3529
195	10	3521	3312
195	12	6604	6837
195	13	7049	6786
195	14	6825	7700
195	15	7682	7047
195	16	7202	7417
195	18	8278	9036
195	20	8583	8837
195	21	8871	9602
195	22	9251	9403
195	23	9600	10022
195	25	10020	10226
195	26	11229	10024
195	27	10659	10946
195	28	10944	11318
195	30	12449	12246
195	32	13212	12505
195	33	12558	12773
195	35	13673	14011

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
195	36	14811	14143
195	38	16061	16363
195	39	16320	16799
195	40	16515	16333
196	1	608	1411
197	9	9269	9553
200	2	1103	249
200	3	1335	1033
200	4	1769	1284
200	5	2124	1747
200	6	2792	2106
200	7	3073	2708
200	8	3510	3061
200	9	4126	3467
200	10	4350	4042
200	11	4847	4368
200	14	6487	6182
200	15	6681	6499
200	18	10749	9307
200	20	11787	11464
200	22	12859	12410
201	1	509	105
201	3	3704	3237
202	7	5296	4817
205	2	117	323
205	5	1669	2148
206	2	546	196
206	3	841	632
206	4	1622	777
206	9	5466	5035
209	1	472	86

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
209	3	1510	1280
210	3	3175	2363
210	6	5281	4868
210	8	5619	6002
211	4	1708	3756
212	1	919	2
213	2	1107	1826
214	2	2106	1237
214	4	3677	3132
217	6	3548	3162
218	1	1	1218
218	3	2731	3378
218	5	4188	4667
219	3	1386	910
219	4	1595	1344
220	2	794	1144
221	1	110	295
221	2	326	880
221	4	1496	1825
221	5	1907	2200
221	6	2169	2555
221	8	3425	4246
221	9	4233	5111
221	12	6419	6757
221	13	6751	6987
221	14	6911	7120
221	16	7400	7909
221	17	7963	8199
221	19	8597	9079
222	17	11376	11597
223	6	5328	5008

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
223	12	12189	13307
223	13	13291	13716
223	14	13601	13434
223	17	15331	15068
223	19	15940	17160
223	21	17710	19089
223	23	19800	20708
223	25	22857	22027
223	26	22757	23365
225	1	756	394
225	5	3793	2945
226	1	141	536
226	2	521	871
228	8	5473	4835
229	7	6749	6057
232	2	1461	910
233	5	3359	3063
233	11	7226	7456
236	1	3	482
237	1	1	219
237	3	1197	991
237	5	2009	2329
237	6	2319	3056
237	8	3261	3701
237	10	3900	4763
237	11	4730	4963
238	11	9966	9238
238	19	16613	17728
238	29	26812	27663
239	2	1576	4245
239	5	6393	6956

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
239	6	6902	7237
240	5	1537	1809
241	1	228	1040
242	9	6581	7015
242	10	6988	7368
242	12	7488	7928
245	2	1670	1251
247	2	1558	1812
250	4	3210	2998
251	1	622	2
252	3	2598	2383
252	4	2911	2564
253	1	1	345
253	2	359	898
254	1	2	307
254	3	318	4
256	5	3768	4040
256	7	7292	6639
256	9	9589	8465
257	2	992	294
257	4	4528	3596
257	7	6894	6718
257	8	7252	6884
257	9	7986	7231
258	2	544	804
258	3	1224	2921
258	4	2964	2728
258	5	2919	3752
258	6	4120	5298
261	1	3	362
264	1	582	361

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
264	2	881	561
264	3	1367	879
264	4	1966	1361
264	5	2316	1945
264	6	2636	2295
264	7	3194	2634
264	8	3531	3055
265	2	398	817
265	4	1583	1071
265	6	3293	3009
265	7	3186	3046
266	1	451	2
266	4	1983	2225
266	7	2540	2325
268	1	798	1223
268	2	1912	1265
270	4	3977	4186
270	6	4397	4573
271	5	2719	3066
271	6	3041	3352
271	9	6278	5862
271	10	6550	5993
271	14	10291	10004
272	3	1870	1199
272	4	3378	1831
276	5	2350	1994
276	8	3702	3103
276	9	4441	3692
276	10	4595	4416
276	12	8173	7382
276	14	10001	9762

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
276	15	11065	9890
276	17	11642	11250
276	19	12892	12503
276	21	13302	13099
276	22	13663	13271
276	23	13995	13642
276	25	15065	14211
276	27	16293	15955
276	29	18482	16563
276	31	19951	19016
279	3	1469	1675
279	4	1600	1923
279	5	2269	2105
279	10	7698	7279
280	3	3138	2968
281	4	2055	2552
282	1	316	2
282	2	456	1232
282	3	1957	1346
283	1	1	450
283	3	1098	1556
283	5	2062	2238
283	7	3127	3312
286	3	2883	2698
287	4	2359	2180
290	10	8820	9074
290	11	9008	9172
291	2	1103	855
291	3	2622	1123
292	1	2	283
292	2	701	330

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
292	5	2459	2866
292	7	4252	4995
292	9	6704	7096
292	10	7066	7827
292	12	8377	8622
292	15	11502	12674
292	17	13326	13727
292	18	13738	14778
294	1	117	623
294	2	905	723
294	6	2496	2272
295	7	4274	4510
300	4	3525	3337
301	6	6714	4852
301	13	10150	9914
301	16	11316	11657
301	18	13199	14398
301	19	15724	14657
306	3	1135	2727
306	4	2742	4025
306	5	4004	4552
306	6	4527	5117
306	7	5131	5466
306	9	5642	5968
306	11	7000	8013
306	12	7926	8138
306	13	8180	8908
306	14	8899	9120
306	15	9118	9510
306	16	9508	9963
306	17	9964	11313

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
306	18	11319	11570
306	19	11540	11707
306	20	11626	11856
310	2	1126	176
310	5	4215	3556
311	4	5671	6006
311	5	6173	6778
311	6	6833	7225
311	7	7236	7520
311	8	7492	7926
312	2	859	1506
312	3	1449	1808
312	4	2043	2306
313	4	3568	3122
319	1	3	881
319	2	832	1185
321	1	638	898
321	4	1862	2131
321	5	2168	2548
321	6	2470	3159
321	7	3069	3395
321	8	3461	3733
324	1	3	692
324	2	867	1592
324	4	2392	3021
327	6	5052	5213
330	5	3745	3464
333	2	998	717
333	3	947	1534
335	2	1024	521
338	11	8869	8591

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
340	5	3931	3608
341	6	3484	3155
341	7	4348	3482
341	8	6419	4332
341	10	9264	7672
341	11	10777	9245
341	12	12026	10779
343	1	459	262
343	4	3905	2661
345	4	3467	3201
345	14	15320	16447
345	16	18409	18927
345	18	19974	20465
347	1	763	1155
350	5	3273	2980
351	1	693	280
351	2	1268	654
351	3	1716	1222
353	4	2749	2546
354	1	2	298
355	16	8911	9399
355	19	12476	12904
355	22	15766	15608
355	23	17165	17461
355	25	18313	19104
355	26	19092	19598
355	27	19692	19495
355	28	19734	20198
355	29	20196	20471
356	2	2204	1536
356	4	2887	2537

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
356	5	3167	2859
357	1	381	4
360	3	3167	2877
361	1	7	909
363	1	1405	167
363	6	7178	8404
364	1	41	331
366	2	1386	1598
367	19	8690	8941
368	4	1786	1947
369	4	1652	1428
372	6	5262	4534
376	2	625	293
377	1	331	2
379	4	2975	3142
382	3	2951	3277
382	4	4183	3320
383	6	6158	5637
386	9	5725	6027
387	2	486	980
390	2	1668	2057
390	3	3499	2867
391	1	2	154
392	5	5163	5387
394	1	1	375
394	8	6437	7585
394	9	7542	7967
394	11	10354	10713
395	5	1957	2229
395	9	3869	4216
395	11	4571	4960

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
398	1	395	1180
399	7	5691	6134
399	10	7662	7820
399	14	10111	9845
399	22	16699	16481
399	29	28519	28244
401	1	189	4
401	2	178	1044
401	3	1038	2141
401	5	3517	3939
402	3	919	1269
404	1	578	12
405	1	293	643
405	3	1926	1501
407	1	80	406
407	4	3188	3670
408	5	3037	2681
408	6	3786	3475
410	2	811	1092
413	2	742	1314
413	3	1275	1532
414	2	908	678
414	3	1137	1889
414	4	2738	1959
416	3	1945	1709
418	1	3	350
418	2	331	930
419	2	619	296
419	4	937	773
419	5	1305	910
419	6	1183	1521

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
419	7	1859	1299
419	8	2170	1850
419	9	2483	2160
419	10	3399	2470
419	11	3708	3397
420	3	1649	1452
421	6	3983	3510
424	1	797	3
424	2	513	851
424	3	1029	733
424	6	1859	1551
424	7	3076	2780
425	1	52	384
425	2	1031	777
425	3	1127	1936
427	2	1488	1114
427	3	2114	1464
430	2	1334	1489
431	1	420	196
431	2	634	269
432	2	1133	1372
432	3	2014	1439
432	6	3869	3378
433	1	292	2007
435	1	706	131
435	2	1730	1047
439	1	1	627
441	1	1	513
441	7	10592	7974
443	1	31	744
447	2	744	322

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
449	1	3	212
449	2	471	286
449	3	551	393
451	1	823	314
452	2	322	714
452	6	2806	3342
452	7	3358	3792
454	1	1033	2
455	3	3214	3837
455	5	4078	4488
455	6	4965	4117
455	8	5123	5473
457	1	940	35
461	2	476	691
461	4	1548	1991
461	5	2322	1948
461	6	2664	2449
462	5	2810	2064
464	2	2162	1530
465	1	1762	38
465	3	2373	2050
467	2	652	1260
467	3	1149	1442
469	2	922	1101
470	2	971	1768
473	2	450	220
475	1	1	969
477	2	1064	843
482	1	1	534
484	1	130	543
484	2	1320	1159

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
487	2	1258	1929
488	2	509	162
488	4	2247	1945
489	1	1	396
489	2	560	255
490	2	1096	458
491	5	5167	4433
491	6	5975	5247
491	7	6811	6041
494	1	650	3
497	5	3351	3536
497	8	4757	4308
497	10	5229	5086
497	11	5967	5671
499	1	663	247
502	2	1324	851
504	1	3	650
507	2	727	906
507	3	840	1010
510	3	2056	2574
512	2	854	300
514	2	1067	669
518	5	3119	2970
520	1	3	467
520	2	452	231
520	4	2218	1859
521	2	988	821
522	1	409	885
524	1	579	4
525	1	1	144
525	2	86	352

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
529	2	5731	6147
533	1	1044	157
536	3	587	1462
539	7	6180	6662
540	1	198	476
543	3	2179	1835
543	4	2404	2177
543	7	3924	3700
544	2	1004	870
546	2	497	324
547	3	717	965
549	2	371	135
550	1	527	3
550	2	864	709
550	3	1540	1277
550	4	2039	1509
552	5	4681	5073
552	8	8390	8223
555	1	470	267
560	1	635	210
560	2	834	514
563	2	1215	1469
564	1	8	511
564	2	1019	555
564	3	577	744
565	1	321	4
565	5	1266	1619
567	2	1055	531
571	3	1149	886
573	1	208	666
573	2	651	1148

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
573	5	2558	2809
575	1	262	2
584	1	268	110
584	4	1310	795
584	5	1329	1574
586	1	771	4
588	1	346	56
588	2	1078	434
589	1	1	555
591	1	217	2
592	2	674	868
593	1	190	2
593	3	1035	1268
601	1	77	274
601	2	172	576
602	2	759	415
604	6	2868	2416
606	1	271	798
607	2	633	797
613	1	420	82
616	2	593	435
616	4	975	730
619	3	641	817
620	1	863	3
621	2	1493	2014
627	1	113	763
628	1	2	163
631	1	1	516
631	3	1715	1521
633	1	280	2
634	3	1139	1387

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
637	2	1613	738
637	3	1597	2208
637	4	2242	2694
637	7	3550	4545
637	9	4767	5171
639	1	175	2
640	2	468	689
643	1	496	320
645	1	1	537
645	2	539	1024
647	1	64	855
647	2	1419	895
649	1	2	364
651	1	539	3
653	2	738	550
656	8	7784	8587
657	2	1356	967
657	3	1708	1376
661	1	2	244
664	3	1149	820
672	1	546	10
673	2	1207	1827
676	1	443	790
679	1	998	219
682	3	749	1171
685	1	176	511
685	2	498	199
685	3	480	947
685	4	1000	1443
686	4	1567	2001
686	5	3238	1712

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
686	7	2965	3435
686	8	3441	3067
686	9	3752	3339
686	10	3530	3826
688	2	628	894
689	2	582	331
690	1	275	90
690	2	487	248
696	1	239	9
696	2	1237	233
696	3	1424	1200
697	1	20	520
698	1	29	313
698	2	217	483
701	5	1061	1534
707	2	855	538
709	1	1	675
710	1	3	416
712	1	674	96
713	1	933	139
713	2	1125	1436
716	2	1226	765
721	1	3	371
726	1	543	94
729	1	19	210
731	1	532	2
736	2	309	644
738	1	561	4
740	1	488	3
749	2	20	475
751	1	1	456

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
751	2	454	774
753	1	76	729
754	1	761	21
755	2	345	539
756	1	1	375
764	2	528	1088
772	1	1	558
772	2	432	866
775	1	706	2
778	2	992	834
780	1	52	351
782	1	3	557
783	1	28	609
791	1	1	582
791	2	859	641
791	3	1235	711
797	1	2	289
797	2	287	3
801	2	598	191
805	1	1	414
806	1	392	3
810	1	3	317
810	2	407	3
815	2	443	282
819	1	39	668
830	1	291	4
830	2	476	162
834	1	561	46
834	2	953	453
837	1	3	317
837	2	320	589

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
839	1	1	753
841	1	1	489
855	1	308	3
861	1	1	330
863	1	451	221
870	1	21	503
890	2	1548	1255
895	1	3	140
896	1	2	400
897	2	244	498
902	1	1	300
904	1	294	4
910	1	143	3
917	1	36	518
918	1	3	167
918	2	116	373
920	2	243	515
922	1	669	259
926	1	2	394
927	1	119	556
928	1	493	179
930	1	526	344
933	2	257	418
936	2	243	683
937	1	341	3
942	1	58	228
945	1	318	4
953	1	254	48
959	1	1198	164
959	2	1740	1123
963	2	462	232

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
965	1	403	2
969	1	360	4
970	3	673	314
972	1	3	470
973	1	2	700
974	1	2	235
974	3	270	467
981	2	154	405
984	3	164	337

SEQUENCE LISTING PLACE INDICATOR

PAGES 280 TO 2076, WHICH ARE THE COMPLETE SEQUENCE LISTINGS FOR THIS APPLICATION ARE LOCATED AFTER THE DESCRIPTION, CLAIMS, ABSTRACT & DRAWINGS.

(i) GENERAL INFORMATION:

(i) APPLICANT: Charles Kunsch
Patrick J. Dillon
Steven C. Barash

(ii) TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

(iii) NUMBER OF SEQUENCES: 982

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.

(B) STREET: 9410 Key West Avenue

(C) CITY: Rockville

(D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: herewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: A. Anders Brookes

(B) REGISTRATION NUMBER: 36,373

(C) REFERENCE/DOCKET NUMBER: PB369PCT

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGTCAATCA CTTGCAAGTC GTTTTCTGTC ATATGGCCGA CTAGCTCAGT GACACCAGGA 60

ATATAGCCAC CAGGGAAAAT ATAACGATTA ATCCAAGCAT TTTTAGCCCC ACCTTGTTGG 120

CGACTGATCC CATGAATCAA CGCCGTACCT TTAGGCGCTA AATTCCGCTG AACGACATCA 180

AAATATTCAT GTAGATTTTC CGCACCGACA TGTTCAAACA TCCCAACACT CGTAATATGG 240

TCAAAAGACT CTCCTTTTAA ATCACGATAA TCCATCAATT TGACAGTCAT TCGATCTTGT 300

AGATCTTCTT TTTCTATAAT ATGGCGAATA TGATGAAATT GCTCTTCACT TAATGTAATC 360

CCAGTTGCTT TGGCTCCATA TTCTTTCACC GCAGTTAAAA TTAACGTGCC CCAGCCGCAG 420

CCAATATCCA GTAAAGTGTC GCCCTCTTTG ATAAACAATT TATCTAAAAT ATGATGAACT 480

TTATTCACTT GCGCTTGTTC TAATGTATCT TCAGGCGTTT TAAAATAAGC ACATGAATAC 540

GTCATTGTTT GGTCAAGCCA TTTTTTGTAA AAATCATTTC CTAGATCGTA ATGGCTGTGA 600

ATATCCTCTT GCGAACGTTT TTTTGAATGA CTTTCTTTAG GAAGCCATTT AATAAATTTA 660

GCATTGTGTA AAAAGCTATC CTTTTGGTTA TACACATCAT AAATCAGsGC TTGGATATCG 720

CCTTCGATTT CAATTTTGCG ATCCATGTAG GCTTCCCCTA AAGTTAACGA AGCGTTATTC 780

AGTAAATCCT TCACAGGAAT TTTTTCATTG AATACAATTT TAAAAACCGG ATCCCCCGAC 840

CCTTGCCCAT ACTCTTTGAC GGTACCATCC CAGTATGTGA CTTGTGTCTT TTTTGAAAAA 900

GACCATTTAA ACAGTTGACT GTACGTTTCT TTTTCTAACA TTGCATTCCC TCCATTAAAT 960

ACCATTTGAA GCCAAAACAA AAAGAAGTCG CTTTCCGGTA GTTCGTCAAA ACAAACACCA 1020

CAGTCCGTTC TAAACTGAAG CACAGAAAAG TTATCACCCC TTCTATGTTC CGCTTCTTTT 1080

TTTGCAATTA CAGTTCTATT CTACTCCTCT TTTAAAAATT TGAACATTCT TTTAACGTAA 1140

TACCTACTAT TGTTATTCTT TATCACAAAA AAACTAGAGC CAGTCCTTGA CAGACTCCTC 1200

TAGTTCTAAA TATTATGCTT TCTTACGCAT CCGTTGTTCC GCATGAGTGT AAGCGCCATG 1260

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

A. The indications made below relate to the microorganism referred to in the description on page 8, line 27

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution (*including postal code and country*)

10801 University Boulevard
Manasas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
May 2, 1997	55969

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications, e.g., "Accession Number of Deposit"*)

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

What Is Claimed Is:

1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-982, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-982.

2. The computer readable medium of claim 1 having recorded thereon any one of the fragments of SEQ ID NOS:1-982 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Enterococcus faecalis* genome of commercial importance comprising the following elements:

a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-982;

b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Enterococcus faecalis* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-982 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Enterococcus faecalis* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-

982 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. An isolated protein-encoding nucleic acid fragment of the *Enterococcus faecalis* genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-982 depicted in Tables 2 and 3, or a degenerate variant thereof.

9. A vector comprising any one of the fragments of the *Enterococcus faecalis* genome of claim 8.

10. An isolated fragment of the *Enterococcus faecalis* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading of claim 8.

11. A vector comprising any one of the fragments of the *Enterococcus faecalis* genome of claim 8.

12. An organism which has been altered to contain any one of the fragments of the *Enterococcus faecalis* genome of claim 8.

13. An organism which has been altered to contain any one of the fragments of the *Enterococcus faecalis* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule to a a nucleic acid molecule of claim 10.

15. An isolated polypeptide encoded by any of the fragments of the *Enterococcus faecalis* genome of claim 8.

16. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 15.

17. An antibody which selectively binds to any one of the polypeptides of claim 15.

18. A method for producing a polypeptide in a host cell comprising the steps of:

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Enterococcus faecalis* genome of claim 8, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

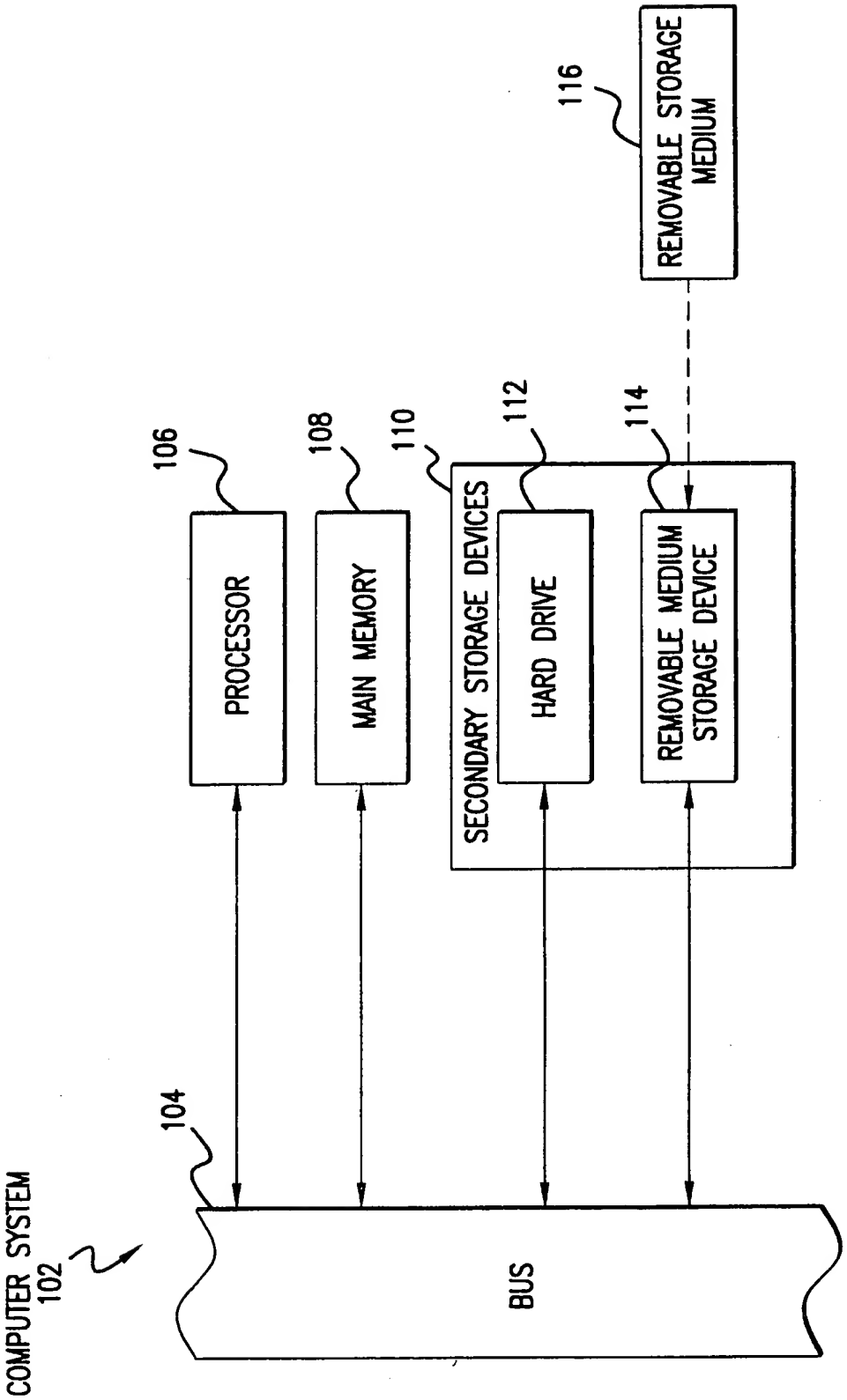

COMPUTER SYSTEM
102
104
BUS
106
PROCESSOR
108
MAIN MEMORY
110
SECONDARY STORAGE DEVICES
112
HARD DRIVE
114
REMOVABLE MEDIUM STORAGE DEVICE
116
REMOVABLE STORAGE MEDIUM

FIG. 1

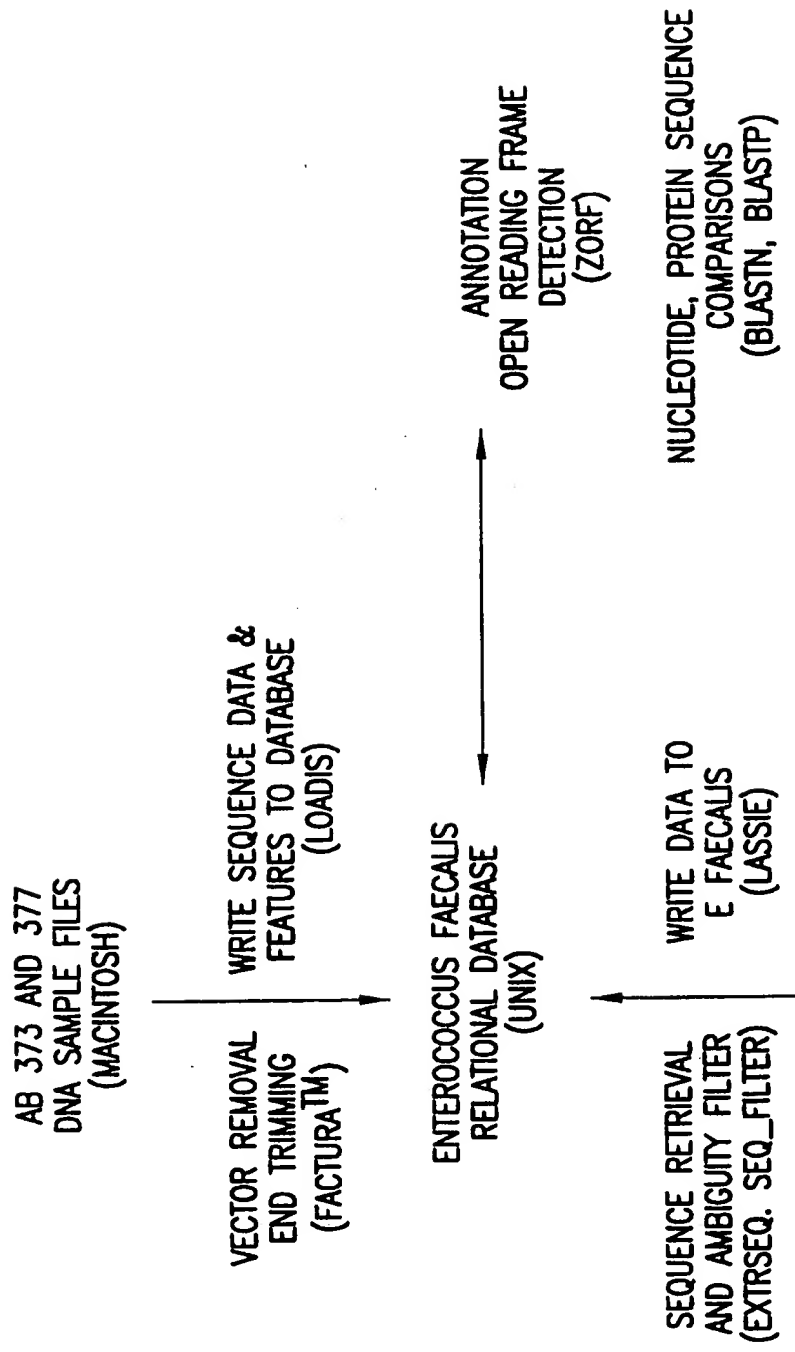

AB 373 AND 377
DNA SAMPLE FILES
(MACINTOSH)
VECTOR REMOVAL
END TRIMMING
(FACTURA™)
WRITE SEQUENCE DATA &
FEATURES TO DATABASE
(LOADIS)
ENTEROCOCCUS FAECALIS
RELATIONAL DATABASE
(UNIX)
ANNOTATION
OPEN READING FRAME
DETECTION
(ZORF)
NUCLEOTIDE, PROTEIN SEQUENCE
COMPARISONS
(BLASTN, BLASTP)
SEQUENCE RETRIEVAL
AND AMBIGUITY FILTER
(EXTRSEQ. SEQ_FILTER)
WRITE DATA TO
E FAECALIS
(LASSIE)
ASSEMBLY
RAPID ASSEMBLY
AND ORDERING OF
THOUSANDS OF SEQUENCES
(TIGR ASSEMBLER)
(ASM_ALIGN)

FIG.2

PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68 | A3

(11) International Publication Number: **WO 98/50555**

(43) International Publication Date: 12 November 1998 (12.11.98)

(21) International Application Number: PCT/US98/08985

(22) International Filing Date: 4 May 1998 (04.05.98)

(30) Priority Data:

60/044,031	6 May 1997 (06.05.97)	US
60/046,655	16 May 1997 (16.05.97)	US
60/066,009	14 November 1997 (14.11.97)	US

(71) Applicant *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: KUNSCH, Charles, A. [US/US]; 4083 Spalding Hollow, Norcross, GA 30092 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US).

(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

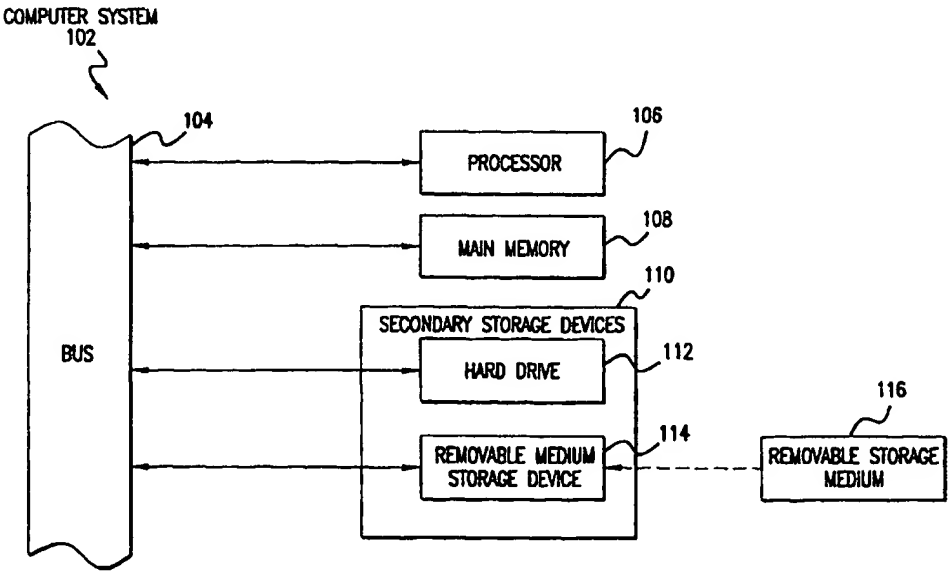
Published

With international search report.

Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(88) Date of publication of the international search report: 14 January 1999 (14.01.99)

(54) Title: *ENTEROCOCCUS FAECALIS* POLYNUCLEOTIDES AND POLYPEPTIDES



(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Enterococcus faecalis*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer–based systems and methods which facilitate its use.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/08985

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/31 C07K14/315 C07K16/12 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 see claims 1-7 ---	1-7
A	EP 0 756 006 A (INST GENOMIC RESEARCH ;UNIV JOHNS HOPKINS (US); UNIV NORTH CAROLIN) 29 January 1997 see claims 1-5 ---	1-7
A	ALTSCHUL S F ET AL: "BASIC LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, vol. 215, 1990, pages 403-410, XP000604562 cited in the application see the whole document ---	1-7
	-/--	

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
12 August 1998	17. 11. 1998

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Lejeune, R

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	W.R. PEARSON AND D.J. LIPMAN: "Improved tools for biological sequence comparison" PROC. NATL. ACAD. SCI., vol. 85, April 1988, NATL. ACAD. SCI.,WASHINGTON,DC,US;, pages 2444-2448, XP002060460 cited in the application see the whole document	1-7
A	EVERS S & COURVALIN P: "Regulation of VanB-Type vancomycin resistance gene expression by the VanS(B)-VanR (B) two-component regulatory system in Enterococcus faecalis V583." JOURNAL OF BACTERIOLOGY, vol. 178, 1996, pages 1302-1309, XP002073904 see abstract	1-7
A	CLARK I M ET AL: "ISOLATION AND SEQUENCE DETERMINATION OF AN IMMUNODOMINANT ANTIGEN FROM ENTEROCOCCUS FAECALIS" SERODIAGNOSIS AND IMMUNOTHERAPY IN INFECTIOUS DISEASE, vol. 5, no. 2, July 1993, pages 85-92, XP002050866 see abstract see figure 3	
A	LOWE A M ET AL: "Cloning of an Enterococcus faecalis endocarditis antigen: homology with adhesins from some oral Streptococci." INFECTION AND IMMUNITY, vol. 63, no. 2, February 1995, pages 703-706, XP002073905 see abstract see figure 2	1-7
A	BURNIE J P & CLARK I: "Diagnosing endocarditis with the cloned 112 kDa antigen of Enterococcus faecalis." JOURNAL OF IMMUNOLOGICAL METHODS, vol. 123, 1989, pages 217-225, XP002074342 see abstract see page 222, column 1, paragraph 2	1-7
P,A	XU Y ET AL: "Enterococcus faecalis antigens in human infections." INFECTION AND IMMUNITY, vol. 65, no. 10, October 1997, pages 4207-4215, XP002073906 see abstract	1-7

INTERNATIONAL SEARCH REPORT

Int\ tional application No.
PCT/US 98/08985

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
See Remark

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7, see subject 1

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequences depicted in SEQ ID nos. 1-982, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-982; a computer-based system for identifying fragments of the Enterococcus faecalis genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequences of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the Enterococcus faecalis genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the Enterococcus faecalis genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-18) partially

An isolated protein-encoding nucleic acid fragment of the Enterococcus faecalis genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising any one of the fragments of SEQ ID no.1 depicted in Tables 2 and 3; an isolated fragment of the Enterococcus faecalis genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frames of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; an isolated polypeptide encoded by any one of the fragments of SEQ ID no.1 depicted in Table

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of SEQ ID no.1 depicted in Table 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and b) isolating said protein;

3-983. Claims: (8-18) partially

Idem as subject 2 but limited to e a c h of the sequences of SEQ ID no. 2 to 982, i.e. invention 3 is limited to the fragments of SEQ ID no. 2 depicted in Tables 2 and 3, invention 4 is limited to the fragments of SEQ ID no. 3 depicted in Tables 2 and 3, and so on.

For the sake of conciseness, the second subject matter is explicitly defined, the other subject matters are defined by analogy hereto.

REMARK:
Although claims 1-4 could, at least partially, be considered as a mere presentation of information, Rule 39.1 (v) PCT, and claims 5-7 at least partially as a program for computers (Rule 39.1(vi) PCT), the search has been carried out as far as possible in our systematic documentation.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 98/08985

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9633276 A	24-10-96	AU 5552396 A	07-11-96
		CA 2218741 A	24-10-96
		EP 0821737 A	04-02-98
EP 0756006 A	29-01-97	CA 2178526 A	08-12-96
		JP 9252787 A	30-09-97